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Om protein - protein search, using sw model

Run on: August 3, 2005, 18:30:15 ; Search time 38 Seconds  
 (without alignments)  
 27.852 Million cell updates/sec

Title: US-10-088-681-1

Perfect score: 60

Sequence: 1 TGSRFSELWTS 11

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1328

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result NO.	Score	Query Match Length	DB ID	Description
1	30	50.0	10 2 C39191	hypothetical prote
2	24	40.0	7 2 PH1602	Ig H chain V-D-J R
3	23	38.3	10 2 T1838	cytochrome-c oxida
4	20	33.3	6 2 B34335	daaa protein - Pro
5	20	33.3	11 2 S05002	corazonin - Americ
6	19	31.7	6 2 PT0519	T-cell receptor be
7	19	31.7	6 2 A41129	neuropeptide GNFR
8	19	31.7	8 2 A41117	acetylcholinester
9	19	31.7	9 2 S3850	Ig heavy chain V
10	18	30.0	9 2 S07241	litorin - Rohde's
11	18	30.0	10 2 C41946	T-cell receptor ga
12	18	30.0	10 2 S53789	neuropeptide Pec-H
13	18	30.0	11 1 LFTWTE	probable trnG lea
14	18	30.0	11 2 S33300	probable substance
15	17.5	29.2	8 2 JS0315	leucokinin V - Mad
16	17	28.3	7 2 PT0586	T-cell receptor be
17	17	28.3	8 2 A44960	neuropeptide Led-C
18	17	28.3	8 2 S0895	hypertrehalosemic
19	17	28.3	8 2 A49823	adipokinetic hormo
20	17	28.3	8 2 A43976	hypertrehalosemic
21	17	28.3	8 2 B43376	hypertrehalosemic
22	17	28.3	8 2 A05169	neuropeptide M-I -
23	17	28.3	10 2 A31571	hypertrehalosemic/
24	16	26.7	4 2 PT0661	T-cell receptor be
25	16	26.7	7 4 I55382	hypothetical pepti
26	16	26.7	8 2 A32523	peptidyl dipeptid
27	16	26.7	8 2 S11545	adipokinetic hormo
28	16	26.7	8 2 A61348	red pigment-concen
29	16	26.7	8 2 A28004	adipokinetic hormo

30	16	26.7	8 2 A39308	glycine reductase
31	16	26.7	9 2 A24244	adipokinetic hormo
32	16	26.7	9 2 PT0315	Ig heavy chain CRD
33	16	26.7	9 2 A43048	cell surface adhes
34	16	26.7	10 2 S08997	hypertrehalosemic
35	16	26.7	10 2 A60421	hypertrehalosemic
36	16	26.7	10 2 S08998	hypertrehalosemic
37	16	26.7	10 2 A23381	hypertrehalosemic
38	16	26.7	10 2 PT0322	Ig heavy chain CRD
39	16	26.7	10 2 T13976	hypertrehalosemic
40	16	26.7	10 2 T11057	hypertrehalosemic
41	16	26.7	10 2 T12303	hypertrehalosemic
42	16	26.7	10 2 T14019	hypertrehalosemic
43	16	26.7	10 2 T17070	hypertrehalosemic
44	16	26.7	10 2 T14043	cytocrome-c oxida
45	16	26.7	10 2 T14054	cytocrome-c oxida
46	16	26.7	10 2 T17066	cytocrome-c oxida
47	16	26.7	10 2 T12321	cytocrome-c oxida
48	16	26.7	10 2 T14219	cytocrome-c oxida
49	16	26.7	11 2 C53552	cytocrome-c oxida
50	16	26.7	11 2 PT0302	cytocrome-c oxida
51	16	26.7	10 2 T12316	cytocrome-c oxida
52	16	26.7	8 2 S10596	cytocrome-c oxida
53	16	26.7	10 2 B27867	cytocrome-c oxida
54	16	26.7	11 2 E61512	cytocrome-c oxida
55	16	26.7	11 2 PT0311	cytocrome-c oxida
56	15	25.0	9 2 G41946	cytocrome-c oxida
61	15	25.0	9 2 JQ0914	MHC class I histoc
62	15	25.0	10 2 PC2372	T-cell receptor ga
63	15	25.0	10 2 E49033	homotetic protein U
64	15	25.0	10 2 F49033	apolipoprotein A-I
65	15	25.0	10 2 H60588	Ig heavy chain CDR
66	15	25.0	11 2 B49164	T-cell receptor ga
67	15	25.0	11 2 PC2372	variant surface g1
68	15	25.0	10 2 A61512	T-cell receptor ga
69	15	25.0	11 2 A61512	variant surface g1
70	14	23.3	5 2 PT0281	Ig heavy chain CRD
71	14	23.3	5 2 PT0308	dihydrofolate redu
72	14	23.3	6 2 A31263	dihydrofolate redu
73	14	23.3	6 2 B31263	palilulanase (EC 3-
74	14	23.3	7 2 PNU649	neuropeptide Led-C
75	14	23.3	8 2 B44960	hypertrehalosemic
76	14	23.3	8 2 S05996	adipokinetic hormo
77	14	23.3	8 2 B48823	T-cell receptor ga
78	14	23.3	8 2 A38887	penalbulin - Adeli
79	14	23.3	9 2 C24180	fibrinogen beta ch
80	14	23.3	9 2 PT0288	Ig heavy chain CRD
81	14	23.3	9 2 PT0299	Ig heavy chain CRD
82	14	23.3	9 2 PT0299	glucan 1,3-beta-1
83	14	23.3	9 2 S56004	translation elonga
84	14	23.3	9 2 PCT074	hypertrehalosemic
85	14	23.3	10 2 JC1416	hypertrehalosemic
86	14	23.3	10 2 S09138	neurokinin A - Chi
87	14	23.3	10 2 JN0024	gonadotropin relea
88	14	23.3	10 2 A49187	Ig heavy chain CRD
89	14	23.3	10 2 PT0289	T-cell receptor al
90	14	23.3	10 2 S23370	slalokinin II - ye
91	14	23.3	10 2 B43581	N-acetylglucosamin
92	14	23.3	10 2 A9581	T-cell receptor be
93	14	23.3	11 2 A53348	cerebellar degener
94	13	22.5	10 2 PH0916	T-cell receptor ga
95	13	21.7	6 2 B5640	T-cell receptor ga
96	13	21.7	6 2 A41946	T-cell receptor ga
97	13	21.7	6 2 A41946	hypothetical prote
98	13	21.7	7 2 S05652	T-cell receptor be
99	13	21.7	7 2 PT0628	tubulin beta-3 cha
100	13	21.7	7 2 S33567	

## ALIGNMENTS

Alignments										
RESULT	1	Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
C39191		hypothetical protein 1 (Tetx 5' region) - <i>Bacteroides fragilis</i>								
		A;Species: <i>Bacteroides fragilis</i>								
		C;Accession: C39191								
		;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993								
		R;Speer, B.S.; Bedzyk, L.; Salyers, A.A.								
		J. Bacteriol. 173, 176-183, 1991								
		A;Status: preliminary; not compared with conceptual translation								
		A;Molecule type: DNA								
		A;Residues: 1-10 <SPE>								
		A;Cross-references: GB: M37699								
Query	QY	1 TGSSFS 6								
	Db	4 TRSFSS 9								
RESULT	2	Query Match 50.0%; Score 30; DB 2; Length 10; Best Local Similarity 62.5%; Pred. No. 19; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;								
		QY	4 FFSELMWS 11							
		2 YFSRDPWTS 9								
PH1602		Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)								
		C;Species: <i>Mus musculus</i> (house mouse)								
		C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999								
		A;Accession: PH1602								
		A;Molecule type: DNA								
		A;Residues: 1-7 <LEW>								
		A;Experimental source: bone marrow pre-B lymphocyte								
		C;Keywords: immunoglobulin								
Query	QY	7 BLW 9								
	Db	4 BLW 6								
RESULT	3	Query Match 33.3%; Score 20; DB 2; Length 6; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
		QY	6 SELWT 10							
		Db	3 SSLWT 7							
T13838		Query Match 33.3%; Score 20; DB 2; Length 11; Best Local Similarity 42.9%; Pred. No. 1.4e+03; Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;								
		QY	5 FSELWS 11							
		Db	5 YSRGWN 11							
RESULT	4	Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
RESULT	5	Query Match 33.3%; Score 20; DB 2; Length 6; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
		QY	7 BLW 9							
		Db	4 BLW 6							
T13838		Query Match 33.3%; Score 20; DB 2; Length 11; Best Local Similarity 42.9%; Pred. No. 1.4e+03; Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;								
		QY	5 FSELWS 11							
		Db	5 YSRGWN 11							
RESULT	6	Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							
PT0519		Query Match 38.3%; Score 23; DB 2; Length 10; Best Local Similarity 83.3%; Pred. No. 3.6e+02; Mismatches 1; Indels 0; Gaps 0;								
		QY	1 TGSSFS 6							
		Db	4 TRSFSS 9							

A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-6 <PFE>  
 A;Experimental source: adult thymus, strain BALB/c  
 C;Keywords: T-cell receptor

Query Match 31.7%; Score 19; DB 2; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	6 SELW 9
Db	2 SSILW 5

RESULT 7

A43129 7 neuropeptide GNPFPRamide - tapeworm (*Moniezia expansa*)  
 C;Species: *Moniezia expansa*  
 C;Date: 10-Nov-1997 #sequence\_revision 14-Nov-1997 #text\_change 09-Jul-2004  
 R;Accession: A43129  
 R;Mauli, A.; Shaw, C.; Halton, D.; Thim, L.  
 Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993  
 A;Title: GNPFPRamide: A novel PRFPRamide-immunoreactive peptide isolated from the sheep t  
 A;Reference number: A43129; MUID:93312289; PMID:8323531  
 A;Accession: A43129  
 A;Molecule type: protein  
 A;Residues: 1-6 <MAU>  
 A;Cross-references: UNIPROT:P41966  
 C;Keywords: amidated carboxyl end; neuropeptide  
 C;6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 31.7%; Score 19; DB 2; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	2 GSFF 5
Db	1 GNPF 4

RESULT 8

A41117 8 acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)  
 C;Species: *Naja naja oxiana* (Asian cobra, Oxus cobra)  
 C;Date: 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 09-Jul-2004  
 C;Accession: A41117  
 R;Kreienkamp, H.J.; Weise, C.; Raba, R.; Ravikumar, A.; Hucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A;Title: Antionic substrates of the catalytic center of acetylcholinesterase from Torpedo a  
 A;Reference number: A41117; MUID:91266772; PMID:2068091  
 A;Accession: A41117  
 A;Statute: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-8 <KRE>  
 A;Cross-references: UNIPROT:Q7LZ27  
 C;Keywords: carboxylic ester hydrolase

Query Match 31.7%; Score 19; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05; Mismatches 2; Indels 0; Gaps 0;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy	6 SELW 9
Db	2 AEWN 5

RESULT 9

S36850 9 Ig heavy chain V region - mouse  
 C;Species: *Mus musculus* (house mouse)  
 C;Date: 05-Jun-1994 #sequence\_revision 01-Dec-1995 #text\_change 05-Nov-1999  
 C;Accession: S36850

R;Jacob, J.; Kelsoe, G. submitted to the EMBL Data Library, July 1992  
 A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl)  
 A;Reference number: S25204  
 A;Accession: S36850  
 A;Statute: preliminary  
 A;Molecule type: nucleic acid  
 A;Residues: 1-9 <JAC>  
 A;Cross-references: EMBL:X67387; NID:950113; PIDN:CA47799.1; PID:651594; PID:g1333871  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 31.7%; Score 19; DB 2; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	2 GSFF 5
Db	6 GSIV 9

RESULT 10

S0241 10 Iitorin - Roehde's leaf frog  
 C;Species: *Phylomedusa rohdei* (Roehde's leaf frog)  
 C;Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 09-Jul-2004  
 C;Accession: S0241  
 R;Barra, D.; Falconieri Brspamer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Brspamer, V.  
 FEBS Lett. 182, 53-56, 1985  
 A;Title: Roehde-Iitorin: a new peptide from the skin of *Phylomedusa rohdei*.  
 A;Reference number: S0241; MUID:85127560; PMID:3838283  
 A;Accession: S0241  
 A;Molecule type: protein  
 A;Residues: 1-9 <BAR>  
 A;Cross-references: UNIPROT:P08946  
 C;Superfamily: gastrin-releasing peptide  
 C;Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid  
 C;6/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 30.0%; Score 18; DB 2; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 2; Indels 1; Gaps 0;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy	7 BLWTS 11
Db	1 QLWAT 5

RESULT 11

C41946 11 T-cell receptor gamma chain (1t.60) - mouse (fragment)  
 C;Species: *Mus musculus* (house mouse)  
 C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
 C;Accession: C41946  
 R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
 Mol. Cell. Biol. 11, 5902-5909, 1991  
 A;Title: Rearrangement and junctional-site sequence analyses of T cell receptor gamma ger  
 A;Reference number: A41946; MUID:92049316; PMID:1658619  
 A;Accession: C41946  
 A;Statute: preliminary; not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-10 <WHE>  
 C;Keywords: T-cell receptor

Query Match 30.0%; Score 18; DB 2; Length 10;  
 Best Local Similarity 28.6%; Pred. No. 2.9e+03; Mismatches 2; Indels 0; Gaps 0;  
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy	5 PSELWTS 11
Db	1 YCAVWSS 7

RESULT 12  
 neuroopeptide Pec-HRH - Platypleura capensis  
 S53779  
 C;Species: *Platypleura capensis*  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C;Accession: S53789  
 R;Gaede, G.; Janssens, M.P.E.  
 Biol. Chem. Hoppe-Seyler 375, 803-809, 1994  
 A;Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehaloseamide-like activity  
 A;Reference number: S53789; NUID:95225985; PMID:7710694  
 A;Accession: S53789  
 A;Molecule type: protein  
 A;Residues: 1-10 <GAE>  
 A;Cross-references: UNIPROT:Q7M465  
 C;Keywords: blocked amino end; blocked carboxyl end  
 LFTWWE  
 probable trpEG leader peptide - *Thermus aquaticus*  
 C;Species: *Thermus aquaticus*  
 C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jul-1999  
 C;Accession: S03315  
 R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.  
*Biochim. Biophys. Acta* 950, 303-312, 1988  
 A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8 trpE and  
 A;Reference number: S03315; NUID:89000781; PMID:2844259  
 A;Accession: S03315  
 A;Molecule type: DNA  
 A;Residues: 1-11 <SRT>  
 A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA05651; PID:948262  
 A;Note: the source is designated as *Thermus thermophilus* HB8  
 C;Genetics:  
 A;Gene: trpL  
 C;Superfamily: probable trpEG leader peptide  
 Query Match 30.0%; Score 18; DB 1; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 6 SEIW 9  
 Db 5 SALW 8  
 RESULT 13  
 S33300  
 probable substance P - smaller spotted catshark  
 C;Species: *Scyliorhinus canicula* (smaller spotted catshark, smaller spotted dogfish)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C;Accession: S33300  
 R;Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.  
*Eur. J. Biochem.* 214, 469-474, 1993  
 A;Title: Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish shark, *Scyliorhinus canicula*  
 A;Reference number: S33300; NUID:93292508; PMID:7685693  
 A;Accession: S33300  
 A;Molecule type: protein  
 A;Residues: 1-11 <WAU>  
 A;Cross-references: UNIPROT:P41333  
 A;Experimental source: brain  
 C;Function:  
 A;Description: may play a physiological role in the regulation of cardiovascular and gas exchange in the dogfish shark  
 A;Note: substance P is derived by post-translational processing of preprotahykinin A  
 C;Keywords: amidated carboxyl end; neuropeptide; tachykinin  
 F;1:1/Modified site: amidated carboxyl end (Met) #status predicted

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GenCore version 5.1.6

OM protein - protein search, using sw model  
Run on: August 3, 2005, 18:18:34 ; Search time 166 Seconds  
(without alignments)  
Sequence: 33.933 Million cell updates/sec

Title: US-10-088-681-1  
Perfect score: 60

Sequence: 1 TGSFFSELWTS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 3223

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Maximum Match 0%  
Listing first 100 summaries

Database : UniProt\_03\_\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	24	40.0	11	2	077895	077895 oreochromis
2	24	40.0	11	2	077896	077896 oreochromis
3	23	38.3	10	2	P92576	bipes bipor
4	23	38.3	11	2	P83537	lactobacill
5	21	35.0	9	2	095953	homo sapien
6	20	33.3	10	2	06LA62	homo sapien
7	20	33.3	11	1	CA42_LITCI	P82092 litoria cic
8	20	33.3	11	1	CORZ_PERAM	P11496 periplaneta
9	20	33.3	11	2	077894	077894 oreochromis
10	20	33.3	11	2	077898	077898 oreochromis
11	20	33.3	11	2	Q65CG7	065CG7 sinaloa tom
12	19	31.7	6	1	FARP_MONEY	P41956 moniezia aer
13	19	31.7	8	2	Q99MNO	Q99MNO muis muscula
14	19	31.7	8	2	Q7LZ27	Q7LZ27 naja oxiana
15	19	31.7	10	2	07TR47	091x47 bos taurus
16	19	31.7	10	2	Q8SHC6	Q8SHC6 furcifer be
17	19	31.7	11	2	Q9UC46	09uc46 homo sapien
18	18	30.0	9	1	LITR_PHYRO	P05946 phylomedusa
19	18	30.0	9	2	Q9H373	Q9H373 hom o sapien
20	18	30.0	9	2	Q8H921	Q8H921 cyanophag
21	18	30.0	9	2	Q9350	090350 gbo virus cl/
22	18	30.0	10	1	AKHX_LOCMI	P81626 locusta mig
23	18	30.0	10	2	Q7M465	Q7m465 platypleura
24	18	30.0	10	2	Q8SHB1	Q8shb1 chlampholema
25	18	30.0	10	2	Q8SHB4	Q8shb4 furcifer ve
26	18	30.0	10	2	Q8SHB7	Q8shb7 furcifer ou
27	18	30.0	10	2	Q8SHC0	Q8shc0 furcifer la
28	18	30.0	10	2	Q8SHC3	Q8shc3 furcifer la
29	18	30.0	11	1	LPW_THETH	P05624 thermus the
30	18	30.0	11	1	TKNA_SCYCA	P41333 scyllorhinus
31	18	30.0	11	2	Q9UE10	Q9uelo homo sapien

Result No.	Score	Query	Match Length	DB	ID	Description
1	24	40.0	11	2	077895	077895 oreochromis
2	24	40.0	11	2	077896	077896 oreochromis
3	23	38.3	10	2	P92576	bipes bipor
4	23	38.3	11	2	P83537	lactobacill
5	21	35.0	9	2	095953	homo sapien
6	20	33.3	10	2	06LA62	homo sapien
7	20	33.3	11	1	CA42_LITCI	P82092 litoria cic
8	20	33.3	11	1	CORZ_PERAM	P11496 periplaneta
9	20	33.3	11	2	077894	077894 oreochromis
10	20	33.3	11	2	077898	077898 oreochromis
11	20	33.3	11	2	Q65CG7	065CG7 sinaloa tom
12	19	31.7	6	1	FARP_MONEY	P41956 moniezia aer
13	19	31.7	8	2	Q99MNO	Q99MNO muis muscula
14	19	31.7	8	2	Q7LZ27	Q7LZ27 naja oxiana
15	19	31.7	10	2	07TR47	091x47 bos taurus
16	19	31.7	10	2	Q8SHC6	Q8SHC6 furcifer be
17	19	31.7	11	2	Q9UC46	09uc46 homo sapien
18	18	30.0	9	1	LITR_PHYRO	P05946 phylomedusa
19	18	30.0	9	2	Q9H373	Q9H373 hom o sapien
20	18	30.0	9	2	Q8H921	Q8H921 cyanophag
21	18	30.0	9	2	Q9350	090350 gbo virus cl/
22	18	30.0	10	1	AKHX_LOCMI	P81626 locusta mig
23	18	30.0	10	2	Q7M465	Q7m465 platypleura
24	18	30.0	10	2	Q8SHB1	Q8shb1 chlampholema
25	18	30.0	10	2	Q8SHB4	Q8shb4 furcifer ve
26	18	30.0	10	2	Q8SHB7	Q8shb7 furcifer ou
27	18	30.0	10	2	Q8SHC0	Q8shc0 furcifer la
28	18	30.0	10	2	Q8SHC3	Q8shc3 furcifer la
29	18	30.0	11	1	LPW_THETH	P05624 thermus the
30	18	30.0	11	1	TKNA_SCYCA	P41333 scyllorhinus
31	18	30.0	11	2	Q9UE10	Q9uelo homo sapien

ALIGNMENTS

Result No.	Score	Query	Match Length	DB	ID	Description
1	24	40.0	11	2	077895	077895 oreochromis
2	24	40.0	11	2	077896	077896 oreochromis
3	23	38.3	10	2	P92576	bipes bipor
4	23	38.3	11	2	P83537	lactobacill
5	21	35.0	9	2	095953	homo sapien
6	20	33.3	10	2	06LA62	homo sapien
7	20	33.3	11	1	CA42_LITCI	P82092 litoria cic
8	20	33.3	11	1	CORZ_PERAM	P11496 periplaneta
9	20	33.3	11	2	077894	077894 oreochromis
10	20	33.3	11	2	077898	077898 oreochromis
11	20	33.3	11	2	Q65CG7	065CG7 sinaloa tom
12	19	31.7	6	1	FARP_MONEY	P41956 moniezia aer
13	19	31.7	8	2	Q99MNO	Q99MNO muis muscula
14	19	31.7	8	2	Q7LZ27	Q7LZ27 naja oxiana
15	19	31.7	10	2	07TR47	091x47 bos taurus
16	19	31.7	10	2	Q8SHC6	Q8SHC6 furcifer be
17	19	31.7	11	2	Q9UC46	09uc46 homo sapien
18	18	30.0	9	1	LITR_PHYRO	P05946 phylomedusa
19	18	30.0	9	2	Q9H373	Q9H373 hom o sapien
20	18	30.0	9	2	Q8H921	Q8H921 cyanophag
21	18	30.0	9	2	Q9350	090350 gbo virus cl/
22	18	30.0	10	1	AKHX_LOCMI	P81626 locusta mig
23	18	30.0	10	2	Q7M465	Q7m465 platypleura
24	18	30.0	10	2	Q8SHB1	Q8shb1 chlampholema
25	18	30.0	10	2	Q8SHB4	Q8shb4 furcifer ve
26	18	30.0	10	2	Q8SHB7	Q8shb7 furcifer ou
27	18	30.0	10	2	Q8SHC0	Q8shc0 furcifer la
28	18	30.0	10	2	Q8SHC3	Q8shc3 furcifer la
29	18	30.0	11	1	LPW_THETH	P05624 thermus the
30	18	30.0	11	1	TKNA_SCYCA	P41333 scyllorhinus
31	18	30.0	11	2	Q9UE10	Q9uelo homo sapien

RESULT 1						
077895	PRELIMINARY;	PRT;	11 AA.			
ID						
AC	O77895;					
DT	01-NOV-1998	(TREMBrel. 08, Created)				
DT	01-NOV-1998	(TREMBrel. 08, Last sequence update)				
DT	01-DEC-2001	(TREMBrel. 19, Last annotation update)				
DE	MHC class II B locus 1.2 (Fragment)					
OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Cichlidae; Oreochromis.					
OC	Actinopterygii; Acanthopterygii; Perciformes; Labroidei; Osteichthyes; Teleostei; Euteleostei; Neoteleostei; Cichlidae; Oreochromis.					
OC	NCBI_TaxID=8128;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	Medline:98315113; PubMed=9649539;					
RA	Malaga-Trillo E., Zalecka-Rutczynska Z., McAndrew B., Vincek V., Piquero F., Sultmann H., Klein J.; "Linkage relationships and haplotype polymorphism among cichlid MHC class II B loci."					
RT	Genetics 149:1527-1537(1998).					
RL	EMBL; AR050005; AAC41344.1; -.					
DR						
FT	NON_TER 1 1					
FT	NON_TER 11 11					
SQ	SEQUENCE 11 AA; 1367 MW; 3F47C9EA772045A3 CRC64;					
Query Match	Best Local Similarity 40.0%; Score 24; DB 2; Length 11; Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;					
QY	4 FFSELWTS 11					
Db	3 FWSLILWA 10					
RESULT 2						
077896	PRELIMINARY;	PRT;	11 AA.			
ID						
AC	O77896;					
DT	01-NOV-1998	(TREMBrel. 08, Created)				
DT	01-NOV-1998	(TREMBrel. 08, Last sequence update)				
DT	01-DEC-2001	(TREMBrel. 19, Last annotation update)				
DE	MHC class II B locus 1.2 (Fragment)					
OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Cichlidae; Oreochromis.					
OC	Actanthomorpha; Acanthopterygii; Perciformes; Labroidei; Cichlidae; Oreochromis.					
OC	NBBI_TaxID=8128;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	Medline:97153826; PubMed=9000757;					
RA	Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.; "Two novel gene orders and the role of light-strand replication in rearrangement of the vertebrate mitochondrial genome.";					
RT	"Replication slippage may cause parallel evolution in the secondary structures of mitochondrial transfer RNAs.";					
RT	Mol. Biol. Evol. 14:91-104(1997).					
RL	EMBL; U71335; ARB48271.1; -.					
DR						
PTR	U71338; T1838;					
GO	GO:0005739; C:mitochondrion; IEA.					
KW	Mitochondrion.					
FT	NON_TER 10 10					
SQ	SEQUENCE 10 AA; 1176 MW; 5B3580C9D5A41A7 CRC64;					
Query Match	Best Local Similarity 83.3%; Score 23; DB 2; Length 10; Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;					
QY	1 TGSFPS 6					
Db	4 TRAFPS 9					
RESULT 3						
P95576	PRELIMINARY;	PRT;	10 AA.			
ID						
AC	P95576;					
DT	01-MAY-1997	(TREMBrel. 03, Created)				
DT	01-MAY-1997	(TREMBrel. 03, Last sequence update)				
DT	01-OCT-2003	(TREMBrel. 25, Last annotation update)				
DE	Cytochrome c oxidase subunit I (Fragment).					
GN	Name=COI;					
OS	Bipes biporus (Baja worm lizard).					
OG	Mitochondrion.					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bipedidae; Bipes.					
OC	Lepidosaurs; Squamata; Scleroglossa; Amphisbaenia; Bipedidae; Bipes.					
OX	NCBI_TaxID=52188;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	Medline:97153826; PubMed=9000757;					
RA	Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.; "Replication slippage may cause parallel evolution in the secondary structures of mitochondrial transfer RNAs.";					
RT	"Replication slippage may cause parallel evolution in the secondary structures of mitochondrial transfer RNAs.";					
RT	Mol. Biol. Evol. 14:91-104(1997).					
RL	EMBL; U71335; ARB48271.1; -.					
DR						
PTR	U71338; T1838;					
GO	GO:0005739; C:mitochondrion; IEA.					
KW	Mitochondrion.					
FT	NON_TER 10 10					
SQ	SEQUENCE 10 AA; 1249 MW; D96C8231B771ADD9 CRC64;					
Query Match	Best Local Similarity 40.0%; Score 24; DB 2; Length 11; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
QY	4 FFSELWTS 9					
Db	3 FWSLILWA 8					

QY	2	GSFFS 6	PRELIMINARY;	PRT;	9 AA.	KW	Ionic channel.
DB	1	GSEFA 5				FT	NON_TER 1
						FT	NON_TER 10
						FT	NON_TER 10
						SEQUENCE	10 AA; 1157 MW;
QY	3	SFFSELW 9	Query Match		33.3%;	Score	20; DB 2; Length 10;
DB	1	SVNSERK 7	Best Local Similarity		57.1%;	Pred. No.	9.1e+03; 0; Mismatches
			Matches		0;	Indels	3; Indels 0; Gaps 0;
RESULT	5						
Q95953							
ID	Q95953						
AC	Q95953;						
DT	01-MAY-1999	(TREMBLrel. 10, Created)					
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)					
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)					
DE	Galactoserebrosidease (EC 3.2.1.46) (Fragment).						
GN	Name=GALC;						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
OX	NBPI_TaxID=606;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TCSSUE-BRIN;						
RA	Lauilli L., torchiana E., Finocchiaro G.;						
RL	Submitted (Nov-1996)	to the EMBL/GenBank/DBJ databases.					
EBML	U77631; AAD15625_1;						
DR	GO:0004336; F:Galactosylceramidase activity; IEA.						
DR	GO: GO_0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.						
DR	GO:005375; P:carbohydrate metabolism; IEA.						
KW	Glycosidase; Hydrolase.						
FT	NON_TER 9						
SO	SEQUENCE 9 AA; 1069 MW; 37482ADC2C699C8 CRC64;						
Query Match	35.0%; Score 21; DB 2; Length 9; Mismatches 3; Conservative 3; Indels 0; Gaps 0;						
Best Local Similarity	37.5%; Pred. No. 1.e+05; Mismatches 3; Conservative 3; Indels 0; Gaps 0;						
QY	2	GSFSELM 9					
Db	2 GFWVADLW 9						
RESULT	6						
Q9LA62							
ID	Q9LA62	PRELIMINARY;	PRT;	10 AA.			
AC	Q9LA62;						
DT	05-JUL-2004	(TREMBLrel. 27, Created)					
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)					
DE	Amiloride-sensitive epithelial sodium channel gamma subunit (Fragment).						
GN	Name=SCNN1G;						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Etheria; Primates; Catarrhini; Hominidae; Homo.						
NCBI_TaxID=9606;	[1]						
RP	SEQUENCE FROM N.A.						
RA	Thomas C.P., Doggett N.A., Fisher R., Stokes J.B.;	MDDLINE=96421599; PubMed=8824247; DOI=10.1074/jbc.271.42.26062;					
RT	"Genomic organization and the 5' flanking region of the gamma subunit of the human amiloride-sensitive epithelial sodium channel.",	J. Biol. Chem. 271:26062-26066(1996).					
RT	[2]						
RP	SEQUENCE FROM N.A.	MDDLINE=98356780; PubMed=9854208;					
RA	Ludwig M., Bolkenius U., Wickett L., Maruyan P., Bidlingmaier F.;	Ludwig M., Bolkenius U., Wickett L., Maruyan P., Bidlingmaier F.;					
RT	"Structural organization of the gene encoding the alpha-subunit of the human amiloride-sensitive epithelial sodium channel.",	Human Genet. 102:576-581(1998).					
RL	DR: 292982; CAB07506_1; -						
DR	GO; GO_0005216; F:ion channel activity; IEA.						
QY	1	TGSFF 5					
Db	5 TGSHF 9						
RESULT	8						
CORZ_PERAM							
ID	CORZ_PERAM	STANDARD;	PRT;	11 AA.			
AC	P11496;						
DT	01-OCT-1989	(Rel. 12, Created)					
DT	01-FEB-1994	(Rel. 28, Last sequence update)					
DT	01-JUL-2004	(Rel. 44, Last annotation update)					
DE	Corazonin.						
OS	Periplaneta americana (American cockroach).						
OC	Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;						
OC	Blattidae; Periplaneta.						

OX	NCBI_TaxID=6978;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN	[1]	OC	Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
RP	SEQUENCE.	OC	Acanthomorpha; Acanthopterygii; Perciformes; Labroidei;
RC	TISSUE-Corpora cardiaca;	CC	Cichlidae; Osteochromis.
RX	Medline=8935572; PubMed=2753132; DOI=10.1016/0014-5793(89)80727-6;	RA	NCBI_TaxID=8128;
RA	"Isolation and structure of corazonin, a cardioactive peptide from the American cockroach.,"	RN	[1]
RT	Amidation; Direct protein sequencing; Neuropeptide;	RP	SEQUENCE FROM N.A.
RL	TREMBL: 250:231-244(1989).	RX	Medline=98315113; PubMed=9649539;
CC	-I FUNCTION: Cardioactive Peptide. Corazonin is probably involved in the physiological regulation of the heart beat.	RA	Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincsek V., Figueira P., Sultmann H., Klein J.;
CC	-! SUBCELLULAR LOCATION: Secreted.	RT	"Linkage relationships and haplotype polymorphism among cichlid MHC Class III B loci.";
DR	PIR; S05002; S05002.	RT	Genetics 149:1527-1537(1998).
KW	Pyrrolidone carboxylic acid.	RL	EMBL; AF050008; AAC41347.1; -.
FT	MOD_RES 1 1	FT	NON_TER 1 1
FT	MOD_RES 11 11	FT	NON_TER 11 11
SQ	SEQUENCE 11 AA; 1387 MW; CTGFF3D6415B46 CRC64;	SQ	SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;
OY	Query Match 33.3%; Score 20; DB 1; Length 11; Best Local Similarity 42.9%; Pred. No. 1e+04; Matches 3; Conservative 2; Indels 0; Gaps 0;	OY	Query Match 33.3%; Score 20; DB 2; Length 11; Best Local Similarity 50.0%; Pred. No. 1e+04; Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db	5 FSPBLWTS 11	Db	3 FMSIVW 8
RESULT 9		RESULT 11	
ID	077894	ID	065CG7
AC	077894; PRELIMINARY; PRT; 11 AA.	AC	065CG7; PRELIMINARY; PRT; 11 AA.
DT	01-NOV-1998 (TREMBLrel. 08, Created)	DT	25-OCT-2004 (TREMBLrel. 28, Created)
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)	DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	DE	Transcriptional activator (Fragment).
DE	MHC class I B locus 112 (Fragment).	GN	Name=AC22;
OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).	OS	Sinaloa tomato leaf curl virus.
OC	Eukaryota; Metazoa; Chordata; Buteleostomi; Teleostei; Neoteleostei; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Labroidei; Cichlidae; Osteochromis.	OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC	NCBI_TaxID=8128;	OX	NCBI_TaxID=71186;
RN	[1]	RN	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	RC	STRAIN=N13;
RX	Medline=98315113; PubMed=9649539;	RA	Rojas A., Kvarnstedt A., Rodriguez D., Valkonen J.P.T.;
RA	Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincsek V., Figueroa P., Sultmann H., Klein J.;	RT	"A mixture of begomoviruses in severe leaf curl-affected tomatoes in Nicaragua."
RA	"Linkage relationships and haplotype polymorphism among cichlid MHC class II B loci.";	RL	Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RT	TREMBL: AF050004; AAC4143.1; -.	DR	EMBL; AJ508781; CAD48523.1; -.
RT	Genetics 149:1527-1537(1998).	FT	NON_TER 1 1
RL	Query Match 33.3%; Score 20; DB 2; Length 11; Best Local Similarity 50.0%; Pred. No. 1e+04; Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	SQ	SEQUENCE 11 AA; 1356 MW; 861BC90602D379D5 CRC64;
DR	FT	OY	Query Match 33.3%; Score 20; DB 2; Length 11; Best Local Similarity 50.0%; Pred. No. 1e+04; Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
EMBL; AF050004; AAC4143.1; -.	FT	Db	4 SFSEELWTS 11
FT	NON_TER 1 1	Db	4 SFSEELWTS 11
SQ	SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;	RESULT 12	
OY	4 FFSEELW 9	ID	FARP_MONEK
Db	3 FMSIVW 8	AC	STANDARD; PRT; 6 AA.
RESULT 10		DT	01-NOV-1995 (Rel. 32, Created)
ID	077898	DT	01-NOV-1995 (Rel. 32, Last sequence update)
AC	PRELIMINARY; PRT; 11 AA.	DT	05-JUL-2004 (Rel. 44, Last annotation update)
AC	01-NOV-1998 (TREMBLrel. 08, Created)	DE	FMRFamide-like neuropeptide FMRFamide.
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)	OS	Moniezia expansa (Sheep tapeworm).
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	OC	Eukaryota; Metazoa; Platyhelminthes; Cestoda; Bucestoda;
DE	MHC class I B locus 12 (Fragment).	OC	Cyclopolyidae; Anoplocephalidae; Moniezia.
OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).	OX	NCBI_TaxID=28841;
OS	[1]	RN	SEQUENCE.

RX	MEDLINE=93312289; PubMed=8323531;	RA	Kreienkamp H.J., Weise C., Raba R., Avnikaar A., Hucho F.;
RA	Mulle A.G., Shaw C., Halton D.W., Thim L.; "GNFRamide: a novel FMRFamide-immunoreactive peptide isolated from the sheep tapeworm, <i>Moniezia expansa</i> ."	RT	"Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo and from cobra venom."
RT		RL	Proc. Natl. Acad. Sci. U.S.A. 88:6117-6121(1991).
RL		DR	PTR; A41117; A41117.
DR	-1- SUBCELLULAR LOCATION: Secreted.	FT	GO; GO:0003990; Facetylcholinesterase activity; IEA.
CC	-1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.	FT	NON_TER 1 1
CC		NON_TER 8 8	SEQUENCE 8 AA; 918 MW; 7P576453769B1DD8 CRC64;
DR	PTR; A43129; A43129.	FT	SEQUENCE 6 AA; 787 MW; 6D949C9C481000 CRC4;
KW	Amidation; Direct protein sequencing; Neuropeptide.	FT	Query Match 31.7%; Score 19; DB 1; Length 6;
FT	MOD RES 6 Phenylalanine amide.	FT	Best Local Similarity 75.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
SQ	SEQUENCE 6 AA; 787 MW; 6D949C9C481000 CRC4;	FT	Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	2 GSFF 5	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
Db	1 GNFF 4	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	Qy	6 SELW 9
Db	2 AEMW 5	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	Qy	6 SELW 9
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	Db	2 AEMW 5
RESULT 13		RESULT 15	
ID	Q99MNO PRELIMINARY; PRT; 8 AA.	ID	Q9TR47 PRELIMINARY; PRT; 10 AA.
AC	Q99MNO; 01-JUN-2001 (TREMBrel 17, Created)	AC	Q9TR47; 01-MAY-2000 (TREMBrel 13, Created)
DT	01-JUN-2001 (TREMBrel 17, Last sequence update)	DT	01-MAY-2000 (TREMBrel 13, Last sequence update)
DT	01-DEC-2001 (TREMBrel 19, Last annotation update)	DT	01-DEC-2001 (TREMBrel 19, Last annotation update)
DE	adenosine deaminase tRNA-specific 1 (Fragment).	DB	Amphotericin homolog (Fragment).
GN	Name=ADAT1;	OS	Bos taurus (Bovine).
OS	Mus musculus (Mouse); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bos.
OC	NCBITaxID=10090; Sequence FROM N.A.	OC	NCBI_TaxID=9913; Sequence FROM N.A.
OX	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE.
RC	STRAIN=129/SVJ;	RX	MEDLINE=96029671; PubMed=7592757; DOI=10.1074/jbc.270.43.25752;
RC	MEDLINE=2121131; PubMed=11331948;	RA	Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X., Nagashima M., Lundt B.R., Vijay S., Nitteck D..
RA	Maas S., Kim Y.G., Rich A.;	RT	"The receptor for advanced glycation end products (RAGE) is a cellular binding site for amphotericin. Mediation of neurite outgrowth and co-expression of rage and amphotericin in the developing nervous system.";
RT	"Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two tRNA synthetases";	RT	J. Biol. Chem. 270:25752-25761(1995).
RT	Manum. Genome 12:387-393(2001).	RL	SEQUENCE 10 AA; 1163 MW; 2B5034453769B18 CRC64;
RL	DR	Query Match 31.7%; Score 19; DB 2; Length 8;	
DR	EMBL; AF328104; AAC1910.1; -.	DB	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
DR	MGI; MGI:1533631; Adat1.	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	NON_TER 8	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
SQ	SEQUENCE 8 AA; 936 MW; F4D05B1AACB1B376 CRC64;	FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	Qy	7 ELWTS 11
Qy	8 LWTS 11	DB	4 EMWNN 8
Db	1 MMWTA 4	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
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FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
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FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
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FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 10;	FT	Query Match 31.7%; Score 19; DB 2; Length 10;
FT	Best Local Similarity 40.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.4e+04; 1; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
FT	Query Match 31.7%; Score 19; DB 2; Length 8;	FT	Query Match 31.7%; Score 19; DB 2; Length 8;
FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;	FT	Best Local Similarity 50.0%; Pred. No. 1.6e+06; 0; Indels 0; Gaps 0;
FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	FT	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;</

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GenCore version 5.1.6  
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OM protein - protein search, using SW model  
Run on: August 3, 2005, 18:17:29 ; Search time 161 Seconds  
(without alignments)  
26.425 Million cell updates/sec

Title: US-10-088-681-1

Perfect score: 60

Sequence: 1 TGSFPELWRS 11

Scoring table: BLOSUM62

Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 494136  
Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:  
1: geneseqD1980s:\*

2: geneseqD1990s:\*

3: geneseqD2000s:\*

4: geneseqD2001s:\*

5: geneseqD2002s:\*

6: geneseqD2003as:\*

7: geneseqD2003bs:\*

8: geneseqD2004as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	#	Match Length	DB ID	Description
1	34	56.7	8	3	AAB09130	Aab09130 Hepatitis Adk09671 Human pap
2	31	51.7	10	8	ADK09671	Adk09671 Human pap
3	31	51.7	10	8	AOK188	Adk0188 Human pap
4	30	50.0	6	6	ABR46515	Abt46515 Staphyloc
5	30	50.0	9	2	AAW72493	Aaw72493 Dengue vi
6	30	50.0	10	19	ADP47198	Adp47198 Human onc
7	29	48.3	7	2	AYA33139	Aay33139 Rabbit ca
8	29	48.3	10	5	AAU33215	Aau33215 Granulocy
9	29	48.3	11	6	ABJ37125	Abj37125 Rhodopsin
10	28	46.7	6	6	ABR46459	Abt46459 Staphyloc
11	28	46.7	7	8	ADRP47302	Adt46302 Androgen
12	28	46.7	9	2	AYA4678	Aay4678 Peptide #
13	28	46.7	10	4	ABBS5959	Abbs5959 Vascular
14	28	46.7	11	3	AYA33379	Aay33379 Binding m
15	28	46.7	11	7	ADP46467	Adp46467 MCP 603
16	27	45.0	6	2	ARR9913	Aar89913 p53/Mdm2
17	27	45.0	6	2	AAW13606	Aaw13606 p53 prote
18	27	45.0	6	3	AAB17074	Abt17074 Mdm/hdm a
19	27	45.0	6	5	ABT2169	Abb73169 Mdm/hdm a
20	27	45.0	6	6	ABR46627	Abt46627 Staphyloc
21	27	45.0	6	6	ABR46507	Abt46507 Staphyloc
22	27	45.0	6	6	ABG73432	Abg73432 Human p53
23	27	45.0	6	7	ADJ13323	Adt13323 Mdm/hdm a
24	27	45.0	6	8	ADJ52957	Adt52957 CH1 delet
25	45.0	6	8	8	ADU51918	Adt51918 CH1 delet

26 27 45.0 7 2 AAR89921 Antibody  
27 27 45.0 7 2 AAB89925 P53 bindi  
28 27 45.0 7 3 AAV57789 TRM-inte  
29 27 45.0 8 8 ADQ28799 Human cel  
30 27 45.0 8 8 ADQ28800 Human cel  
31 27 45.0 9 2 AAW37199 Human onc  
32 27 45.0 9 5 AAE31317 Human HLA  
33 27 45.0 9 5 AAE31316 Human p53  
34 27 45.0 9 8 ADK09130 Human HLA  
35 27 45.0 9 8 ADK09595 Human pap  
36 27 45.0 9 8 ADK09595 Human cel  
37 27 45.0 9 8 ADQ28798 Human HLA  
38 27 45.0 9 8 ADP00098 Human HLA  
39 27 45.0 10 2 AAB89917 Human p53  
40 27 45.0 10 8 AAW13605 Human HLA  
41 27 45.0 10 8 ADP0344 Human HLA  
42 27 45.0 10 8 ADT02867 Human p53  
43 27 45.0 10 8 ADW48959 Human HLA  
44 27 45.0 10 8 ADP47192 Human pho  
45 27 45.0 10 8 ADG90923 Human HLA  
46 27 45.0 10 8 ADP8034 Human HLA  
47 27 45.0 10 8 ADT02867 Human p53  
48 27 45.0 11 2 AAW11231 Human HLA  
49 27 45.0 11 4 AAU37152 Human HLA  
50 27 45.0 11 5 AAU56842 Human Leu  
51 27 45.0 11 5 AAM52269 Miniature  
52 27 45.0 11 8 ADW6486 Human HLA  
53 27 45.0 11 8 ADP0368 Human HLA  
54 26 43.3 5 2 AAB89912 Human HLA  
55 26 43.3 6 5 ABR46403 Staphyloc  
56 26 43.3 8 6 ABPP8083 Amino aci  
57 26 43.3 8 6 ABPP8084 Amino aci  
58 26 43.3 8 6 ABPP8081 Amino aci  
59 26 43.3 8 6 ABPP8082 Amino aci  
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61 61 43.3 8 8 ADP00532 Human apo  
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64 26 43.3 8 8 ADP99992 Human apo  
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71 26 43.3 8 8 ADP54214 Human apo  
72 26 43.3 10 8 ADP94728 Human JAM  
73 26 43.3 10 8 ADP47102 Human JAM  
74 26 43.3 10 8 ADP87303 Human clu  
75 25 41.7 5 7 ABG75141 F laterrit  
76 25 41.7 6 6 ABR46739 Staphyloc  
77 25 41.7 6 6 ABR46531 Staphyloc  
78 25 41.7 6 6 ABR46523 Staphyloc  
79 25 41.7 6 6 ABR46451 Staphyloc  
80 25 41.7 6 6 ABR46519 Staphyloc  
81 25 41.7 7 6 AAB331848 Androgen  
82 25 41.7 8 6 ABP54137 Beta-secr  
83 25 41.7 8 6 ABP54135 Beta-secr  
84 25 41.7 8 6 ABP54139 Beta-secr  
85 25 41.7 8 6 ABP54141 Beta-secr  
86 25 41.7 8 7 ADP47092 YPS1 prot  
87 25 41.7 8 8 ADI02276 Murine Im  
88 25 41.7 9 9 ABG72829 Anti-NKG2  
89 25 41.7 9 5 ABG67520 Human ADP  
90 25 41.7 9 6 ADA23363 Alzheimer  
91 25 41.7 9 7 ADI17228 Phage-dis  
92 25 41.7 9 8 ADK03025 Hepatitis  
93 25 41.7 10 5 ABG70412 CD1/H1 r  
94 25 41.7 10 5 AAB82448 Llama CDR  
95 25 41.7 10 7 ADM07748 Canine im  
96 25 41.7 10 8 ADI34765 Human GPR  
97 25 41.7 10 8 ADP47006 Murine he  
98 41.7

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Adl02276 Murine Im  
Adg75141 F laterrit  
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Adr46519 Staphyloc  
Aae31317 Human p53  
Aav52269 Miniature  
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Adp999





invention for an epitope mapping assay. The invention has developed peptide antigens consisting of fragments of the dengue virus NS1 protein. The peptide antigens can be used for the diagnosis of dengue virus infection by detection of antibodies to the virus, especially in an assay comprising attaching the antigen to a solid support, contacting a serum sample with the support, and detecting bound antibodies with a labelled anti-human antibody or used for preparing vaccines against dengue virus.

CC Sequence 9 AA:  
 Query Match Score 30; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GSFFSELMW 9  
 Db 1 GVFVFINIW 8

RESULT 6  
 AAW37198  
 ID AAW37198 standard; peptide; 10 AA.  
 AC XX  
 AC AAW37198;  
 DT 20-JUL-1998 (first entry)  
 DE Human oncogenic protein MDM2 binding Cys (Acrlid) peptide derivative 2.  
 XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 KW tumour; diagnosis; binding; viral infection.  
 OS Synthetic.  
 OS Homo sapiens.  
 FH Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal acetyl: Sulphydryl side-chain linked  
 to 6-acryloyl-2-(dimethylamino) naphthalene"  
 FT Modified-site 10 /note= "C-terminal amide"  
 FT /note= "C-terminal amide"  
 XX WO9801467-A2.  
 XX PN PR 07-APR-1997; 97GB-00007041.  
 PD 15-JAN-1998.  
 XX PR 04-JUL-1997; 97WO-EP003549.  
 XX PR 05-JUL-1996; 96GB-00014197.  
 PR 07-APR-1997; 97GB-00007041.  
 XX PA (NOV ) NOVARTIS AG.  
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 XX PI Lane D, Boettger V, Boettger A, Picklesay S, Hockeppel H;  
 PI Garcia-Echeverria C, Chene P, Furet P;  
 DR WPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 - useful in, e.g. diagnosis and treatment of cancer and viral infections and identifying binding agents.  
 XX PS Example 2; Page 20; 45pp; English.  
 XX This is a Cys (Acrlid) peptide derivative capable of binding to a human oncogenic protein MDM2. The MDM2 binding peptides can specifically inhibit or block the binding of MDM2 to the human p53 protein, *in vitro* or *in vivo*. Inhibiting the interaction between the p53 and MDM2 can induce growth arrest or apoptosis in tumour cells comprising a wild-type p53 and non-elevated levels of MDM2. The peptides may be used to identify molecules that bind to MDM2 and to identify and design inhibitors of

CC MDM2/p53 binding. They may also be used to purify binding partners especially MDM2, diagnose disease by measuring levels of MDM2 in blood of cancer and leukaemia patients and for treatment or prevention of disease involving p53/MDM2 interactions, especially tumours and viral infections. The peptides can be administered nasally, rectally, orally or by injection. By interfering with MDM2/p53 interaction, the peptides can activate p53 function and accumulation in normal cells. The peptides which mimic the MDM2 binding site in p53, have a significantly greater blocking activity compared with wild-type p53

CC Sequence 10 AA:  
 Query Match Score 30; DB 2; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GSFFSELMW 9  
 Db 2 GPFPSDLW 9

RESULT 7  
 AAY33139  
 ID AAY33139 standard; peptide; 7 AA.  
 AC XX  
 AC AAY33139;  
 DT 16-NOV-1999 (first entry)  
 DE Rabbit carboxylesterase protein fragment #3.  
 XX Carboxylesterase; rabbit; tumour cell; chemotherapy; prodrug;  
 KW disease-specific responsive promoter; CRR-11; APC; resection; recurrence;  
 KW inhibition; bone marrow cell.  
 XX Oryctolagus cuniculus.  
 XX WO942593-A1.  
 XX PR 19-FEB-1998; 98US-0075258P.  
 XX PD 26-AUG-1999.  
 XX PA (SUD-) ST JUDE CHILDREN'S RES HOSPITAL.  
 XX PF 12-FEB-1999; 99WO-US003171.  
 XX DR 19-FEB-1998; 98US-0075258P.  
 XX PI Danks MK, Potter PM, Houghton PJ;  
 XX DR WPT; 1999-540311/45.  
 XX PT New carboxylesterase polypeptide for treatment of tumors.  
 XX PS Example 2; Page 57; 70pp; English.  
 XX This invention describes a novel rabbit carboxylesterase polypeptide (I) capable of metabolizing a chemotherapeutic prodrug and its inactive metabolites into an active drug. The invention also describes a composition comprising (I) and a disease-specific responsive promoter. This composition is useful for sensitizing tumor cells to a chemotherapeutic prodrug (preferably CRT-11 or APC) by transfecting into tumor cells, and contacting the sensitized cells with a chemotherapeutic prodrug to inhibit growth of the tumor cells. The composition can also be administered to the site of tumor resection to inhibit tumor recurrence, and be administered to bone marrow cells to remove tumor cells. The products of the invention are useful for identifying drugs that are inactivated by a carboxylesterase enzyme, and are also useful for identifying compounds containing a COOC ester linkage that are activated by a carboxylesterase enzyme. This sequence represents a fragment of a rabbit carboxylesterase which is described in the method of the invention

CC Sequence 7 AA:  
 Query Match Score 30; DB 2; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GSFFSELMW 9  
 Db 2 GPFPSDLW 9

CC This invention describes a novel rabbit carboxylesterase polypeptide (I) capable of metabolizing a chemotherapeutic prodrug and its inactive metabolites into an active drug. The invention also describes a composition comprising (I) and a disease-specific responsive promoter. This composition is useful for sensitizing tumor cells to a chemotherapeutic prodrug (preferably CRT-11 or APC) by transfecting into tumor cells, and contacting the sensitized cells with a chemotherapeutic prodrug to inhibit growth of the tumor cells. The composition can also be administered to the site of tumor resection to inhibit tumor recurrence, and be administered to bone marrow cells to remove tumor cells. The products of the invention are useful for identifying drugs that are inactivated by a carboxylesterase enzyme, and are also useful for identifying compounds containing a COOC ester linkage that are activated by a carboxylesterase enzyme. This sequence represents a fragment of a rabbit carboxylesterase which is described in the method of the invention

cells expressing G-CSFR on the cell surface (or inside permeabilised cells) as a commercial research reagent for various medical and diagnostic uses or to treat a disease that would benefit from the ability to of a compound to mimic the effects of G-CSF in vivo. The compounds bind specifically to G-CSFR and allow for studies of biological activities mediated by the receptor and for the treatment of diseases, disorders and conditions that would benefit from activating or inactivating G-CSFR. The present sequence is a G-CSFR binding peptide of the invention.

		Query/ Match	Score 29; DB 6; Length 11;
		Best Local Similarity	40.3%; Pred. No. 2 4e+02;
		Matches	Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
OY	7	ELWTS 11	
Db	2	ELWTS 6	
		RESULT 10	RESULT 11
		ABR46459	Score 29; DB 6; Length 11;
		ID ABR46459	Best Local Similarity 100.0%; Pred. No. 2 4e+02;
		AC ABR46459;	Mismatches 0; Indels 0; Gaps 0;
		DT 10-JUN-2003	(first entry)
		DB Staphylococcus aureus CHIPS-related peptide #1649.	XX
		XK CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;	XX
		KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;	XX
		KW inflammation; cardiovascular disease; central nervous system disease;	XX
		KW gastrointestinal disease; skin disease; genitourinary disease;	XX
		KW joint disease; respiratory disease; HIV infection; antiinflammatory;	XX
		KW cardiotonic; cerebroprotective; neuroprotective; nootropic; dermatological;	XX
		KW gynecological; immunosuppressive; anti-HIV.	XX
		OS Staphylococcus aureus.	OS
		OS Synthetic.	Synthetic.
		PN WO2003006048-A1.	PN
		XX PD 10-SEP-2004.	PD
		XX PF 10-FEB-2004; 2004WO-US003774.	PF
		XX PR 12-FEB-2003; 2003US-0446955P.	PR
		XX PA (KARO-) KARO BIO AB.	PA
		XX PI Buehrer BM, Barnett TR;	PI
		XX DR WPI; 2004-653365/63.	DR
		XX PS New polypeptides that bind to the androgen receptor, useful for	PS
		PT diagnosing or treating diseases associated with abnormal levels of	PT
		PT activation of androgen receptor, e.g. prostate cancer, or in biological	PT
		XX research.	XX
		XX Disclosure: SEQ ID NO 20; 46PP; English.	XX
		The present invention describes a polypeptide that binds to the androgen receptor, or a polypeptide that comprises at least 50% amino acid sequence identity to the polypeptide. Also described: (1) methods of analysing the surface conformation of a protein using one or more of the polypeptide sequences mentioned above; (2) methods of identifying modulators of protein function using one or more of the polypeptide sequences mentioned above; (3) a pharmaceutical composition comprising a pharmaceutical carrier and one or more of the polypeptide sequences described above; (4) a peptide that binds to the androgen receptor, the binding being competitively inhibited by the polypeptide described above; (5) a chimeric protein comprising the above polypeptide and at least a portion of a filamentous phage protein, the portion of the filamentous phage protein being sufficient for integration of the chimera protein into the coat of phage particles to display the polypeptide; (6) a diagnostic method of diagnosing a disease in a patient characterised by abnormal levels of activation of androgen receptor, comprising providing a sample of body fluid or tissue of the patient, administering a diagnostic amount of the pharmaceutical composition described above, and assaying the amount of activated androgen receptor in the body fluid or tissue of the patient; and (8) a method of treating a patient suffering from a disease characterised by abnormal levels of activation of androgen receptor, comprising administering to the patient a therapeutic amount of the pharmaceutical composition described above. The androgen receptor interacting polypeptide has cytostatic activity, and can be used in gene therapy. The composition and methods are useful for diagnosing or treating patients suffering from diseases characterised by abnormal levels of activation of androgen receptor, such as prostate cancer. They may also be used in biological research, as therapeutics or for in vitro or in vivo classification of compounds. The present sequence represents an androgen receptor interacting peptide, which is used in the exemplification of the present invention.	CC
		SQ Sequence 6 AA;	CC
		Query/ Match 46.7%; Score 28; DB 6; Length 6;	CC
		Best Local Similarity 66.7%; Pred. No. 1.e+06;	CC
		Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	CC
OY	4	FISSEBLW 9	
Db	1	FFPEIW 6	
		SQ Sequence 7 AA;	XX

				Query Match	46.7%; Score 28; DB 8; Length 7;	KW diagnosis; prognosis; gene therapy.
				Best Local Similarity 71.4%; Pred. No. 1.8e+06; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		XX XX OS Homo sapiens.
Oy	3	SFSELW 9				XX PN WO200165261-A2.
Db	1	SRAELW 7				XX PD 20-SEP-2001.
				RESULT 12		XX XX
				AY04678		PF 14-MAR-2001; 2001WO-GB001106.
				ID AAY04678 standard; peptide; 9 AA.		XX PR 15-MAR-2000; 2000GB-00006785.
				XX AC AAY04678;		PR 24-NOV-2000; 2000GB-00028734.
				XX DT 22-JUN-1999 (first entry)		XX PR 28-NOV-2000; 2000US-00724391.
				XX DE Peptide #13 encoded by Hsdr/M/S gene fragment.		XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
				XX KW Hsdr; Hsds; restriction/modification; bacteriophage; resistance; lactic acid bacterium.		XX PI Herath HMAC, Parekh RB, Rohlf C;
				XX KW Lactococcus lactis.		XX DR WPI; 2001-557937/62.
				XX PN FR22767831-A1.		XX XX
				XX PD 05-MAR-1999.		PT Screening, diagnosis or prognosis of vascular
				XX PR 02-SEP-1997; 97FR-00010885.		PT determining stage of VD and monitoring the effect of VD therapy, for
				XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.		PT comprises analysing body fluid by 2-dimensional electrophoresis for
				XX PT Chopin MC, Clier F, Ehrlich SP, Gautier M, Schouller C;		PT features correlated with VD.
				XX DR WPI; 1999-183265/16.		XX XX
				XX PT Bacteriophage resistance mechanism subunit polypeptides - of lactic acid		PS Claim 6; Page 33; 151pp; English.
				XX CC bacteria, especially lactobacillus lactis.		CC The invention relates to screening, diagnosis or prognosis of Vascular
				XX CC DR		CC Dementia (VD) in a subject comprising analysing body fluid from the
				XX CC PT		CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
				XX CC PT		CC features containing at least one chosen feature whose relative abundance
				XX CC PT		CC correlates with the presence, absence, stage or severity of VD or
				XX CC PT		CC predicts the onset or course of VD, especially detecting in a sample of
				XX CC PT		CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
				XX CC PT		CC protein isoforms (VP18) (ABBS5501-ABSB5695) as fully defined in the
				XX CC PT		CC specification. Detecting VD-associated features and VPI is useful for the
				XX CC PT		CC screening, diagnosis or prognosis of VD, for determining the stage or
				XX CC PT		CC severity of VD, for identifying a subject at risk of VD or for monitoring
				XX CC PT		CC the effect of therapy administered to a subject having VD. Nucleic acids
				XX CC PT		CC encoding a VPI or inhibiting the function of a VPI are useful for the
				XX CC PT		CC treatment of VD and for gene therapy
				XX SQ Sequence 9 AA;		XX XX
				Query Match	46.7%; Score 28; DB 4; Length 10;	Query Match
				Best Local Similarity 71.4%; Pred. No. 3.3e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Best Local Similarity 71.4%; Pred. No. 1.8e+06; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy	3	SFSELW 9		Oy 3	SFSELW 9	Oy 3
Db	1	SRAELW 7		Db 1	SRAELW 7	Db 1
				RESULT 13		RESULT 14
				ABB55959	AY93379	AY93379
				ID ABB55959 standard; peptide; 10 AA.	ID AAY93379 standard; peptide; 11 AA.	ID AAY93379
				XX AC ABB55959;	XX AC AAY93379;	XX AC AAY93379;
				XX DT 15-FEB-2002 (first entry)	XX DT 04-SEP-2000 (first entry)	XX DT 04-SEP-2000 (first entry)
				XX PN WO200025807-A1.	XX PN WO200025807-A1.	XX PN WO200025807-A1.
				XX DE Vasculardementia-associated protein isoform (VPI) 159.	XX PD 11-MAY-2000.	XX PD 11-MAY-2000.
				XX KW vascular dementia; VP; VP-associated protein isoform; VPI; screening;	XX PF 04-NOV-1999; 99WO-US026275.	XX PF 04-NOV-1999; 99WO-US026275.

XX  
 PR 05-NOV-1998; 98US-00186958.  
 XX  
 PA (DYAX-) DYAX CORP.  
 XX  
 PI Whelihan EF;  
 XX  
 DR WPI; 2000-365396/31.  
 PT Human Parvovirus B19 polypeptide binding moiety, used to detect, clear  
 and isolate parvovirus B19 polypeptides from blood and other solutions.  
 XX  
 PS Claim 2; Page 36; 47pp; English.  
 XX  
 AAV93377-94 represent binding moieties for human parvovirus B19 or B19-like polypeptides, particularly VPI or VP2 capsid proteins. AAV93377-85  
 CC are isolated from a TN7 library. AAV93386-89 are isolated from a TN8  
 CC library, and AAV93390-94 are isolated from a TN9 library. The B19 binding  
 CC moieties can be used for detection and clearing of parvovirus B19 and/or  
 CC B19-like polypeptides from any solution which contains them, e.g. blood.  
 CC They may also be used to isolate parvovirus B19 and/or B19-like viruses  
 CC or polypeptides, which may be used in parvovirus vaccines  
 XX  
 SQ Sequence 11 AA;

Query Match Score 28; DB 3; Length 11;  
 Best Local Similarity 46.7%; Pred. No. 3.6e+02;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4 FFSSELWTS 11  
 Db 1 FFCALWPS 8

XX  
 This invention relates to a novel method of walk-through mutagenesis of a  
 CC nucleic acid encoding a polypeptide, which comprises synthesising a  
 CC mixture of oligonucleotides comprising a nucleotide sequence for each  
 CC target region of a prototype amino acid, where each oligonucleotide  
 CC contains, at each sequence position in the target region, a prototype  
 CC nucleotide for synthesis of the prototype amino acid, or a predetermined  
 CC nucleotide that is required for synthesis of the predetermined amino  
 CC acid. The method is useful in producing mutant polypeptides in which the  
 CC overall presence or the predetermined amino acid is limited to one or two  
 CC positions per mutated polypeptide, leaving the remaining amino acids in  
 CC the targeted region intact or as close as possible to the prototype  
 CC sequence. The invention was exemplified using the three complementarity  
 CC determining regions (CDRs) of the heavy chain of the monoclonal antibody  
 CC MPC 603.

SQ Sequence 11 AA;

Query Match Score 28; DB 7; Length 11;  
 Best Local Similarity 46.7%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 3 SFFSELWTS 11  
 Db 1 SYSSSSWSS 9

Search completed: August 3, 2005, 18:38:09  
 Job time : 167 secs

RESULT 15  
 ADP53467  
 ID ADP53467 standard; peptide; 11 AA.  
 XX  
 AC ADP53467;  
 XX  
 DT 12-FEB-2004 (first entry)

XX  
 DE MCPC 603 antibody CDR3 mutant peptide amino acid sequence 10.  
 XX  
 KW walk-through mutagenesis; prototype amino acid; prototype nucleotide;  
 KW mutant polypeptide production; MCPC 603;  
 KW complementarity determining region; CDR; heavy chain; CDR3; mutant;  
 KW muttein.  
 XX  
 OS Unidentified.  
 OS Synthetic.  
 XX  
 PN WO2003089671-A1.  
 XX  
 PD 30-OCT-2003.  
 XX  
 PF 16-APR-2003; 2003WO-US011935.  
 XX  
 PR 17-APR-2002; 2002US-0373686P.  
 XX  
 PA (CREA/) CREA R.  
 PA (CAPP/) CAPPICILLI G.  
 XX  
 PI Crea R., Cappuccilli G;  
 XX  
 DR WPI; 2003-854132/79.

XX  
 PT Walk-through mutagenesis of a nucleic acid encoding a polypeptide, useful  
 PT for producing mutant polypeptides comprising synthesizing oligonucleotides  
 PT comprising a nucleotide sequence for each target region of a prototype  
 PT amino acid.

XX  
 PS Example; Fig 7; 40pp; English.

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Om protein - protein search, using sw model  
Run on: August 3, 2005, 18:32:08 ; Search time 43 Seconds  
(without alignments)  
19.096 Million cell updates/sec

Title: US-10-088-681-1  
Perfect score: 60

Sequence: 1 TGSFFSBLWTS 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues  
Total number of hits satisfying chosen parameters: 125705

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Parents Ab:  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result NO.	Score	Query Match Length	DB ID	Description
1	34	56.7	8 4 US-08-469-260-252	Sequence 252, App
2	34	56.7	8 4 US-08-488-445-252	Sequence 252, App
3	34	56.7	8 4 US-08-467-344-252	Sequence 252, App
4	34	56.7	8 4 US-08-424-550-252	Sequence 252, App
5	30	50.0	6 1 US-08-424-957-6	Sequence 6, Appl
6	30	50.0	6 3 US-08-035-686-6	Sequence 6, Appl
7	30	50.0	11 1 US-08-424-957-42	Sequence 42, Appl
8	30	50.0	11 3 US-08-424-957-42	Sequence 42, Appl
9	29	48.3	7 4 US-09-595-682-10	Sequence 10, Appl
10	29	48.3	10 4 US-09-620-091-28	Sequence 28, Appl
11	28	46.7	11 3 US-09-180-958-6	Sequence 6, Appl
12	28	46.7	11 3 US-09-669-271-6	Sequence 6, Appl
13	28	46.7	11 4 US-09-881-276-6	Sequence 6, Appl
14	27	45.0	6 1 US-09-277-660-2	Sequence 2, Appl
15	27	45.0	6 1 US-08-424-957-2	Sequence 2, Appl
16	27	45.0	3 0 US-09-035-686-2	Sequence 19, Appl
17	27	45.0	4 0 US-09-081-975-1	Sequence 1, Appl
18	27	45.0	6 4 US-09-428-082-130	Sequence 130, Appl
19	27	45.0	6 4 US-09-732-384-4	Sequence 6, Appl
20	27	45.0	7 1 US-09-277-660-27	Sequence 27, Appl
21	27	45.0	7 1 US-08-424-957-15	Sequence 15, Appl
22	27	45.0	7 1 US-08-424-957-19	Sequence 19, Appl
23	27	45.0	7 3 US-09-035-686-15	Sequence 1, Appl
24	27	45.0	7 3 US-09-035-686-19	Sequence 19, Appl
25	27	45.0	10 1 US-08-277-660-7	Sequence 7, Appl
26	27	45.0	10 1 US-08-424-957-11	Sequence 11, Appl
27	45.0	10 1 US-08-424-957-18	Sequence 18, Appl	

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23	31	45.0	11 1 US-08-277-660-10	Sequence 10, Appl
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23	33	45.0	11 1 US-08-277-660-12	Sequence 12, Appl
23	34	45.0	11 1 US-08-277-660-13	Sequence 13, Appl
23	35	45.0	11 1 US-08-277-660-19	Sequence 19, Appl
23	36	45.0	11 1 US-08-277-660-20	Sequence 20, Appl
23	37	45.0	11 1 US-08-424-957-17	Sequence 17, Appl
23	38	45.0	11 1 US-08-424-957-23	Sequence 23, Appl
23	39	45.0	11 1 US-08-424-957-24	Sequence 24, Appl
23	40	45.0	11 1 US-08-424-957-25	Sequence 25, Appl
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23	42	45.0	11 1 US-08-424-957-32	Sequence 32, Appl
23	43	45.0	11 1 US-08-424-957-33	Sequence 33, Appl
23	44	45.0	11 1 US-08-424-957-34	Sequence 34, Appl
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23	54	45.0	11 1 US-09-035-686-34	Sequence 44, Appl
23	55	45.0	11 1 US-09-035-686-36	Sequence 45, Appl
23	56	45.0	11 1 US-09-035-686-43	Sequence 46, Appl
23	57	45.0	11 1 US-09-603-052-5	Sequence 47, Appl
23	58	43.3	5 3 US-09-035-686-45	Sequence 48, Appl
23	59	43.3	5 3 US-09-035-686-45	Sequence 49, Appl
23	60	41.7	9 1 US-08-288-405A-8	Sequence 50, Appl
23	61	41.7	11 1 US-08-424-957-44	Sequence 51, Appl
23	62	41.7	11 1 US-08-424-957-45	Sequence 52, Appl
23	63	41.7	11 1 US-08-424-957-46	Sequence 53, Appl
23	64	41.7	11 1 US-09-035-686-44	Sequence 54, Appl
23	65	41.7	11 3 US-09-035-686-45	Sequence 55, Appl
23	66	41.7	11 3 US-09-035-686-46	Sequence 56, Appl
23	67	41.7	11 3 US-09-630-202A-36	Sequence 57, Appl
23	68	40.0	7 4 US-09-036-749A-36	Sequence 58, Appl
23	69	40.0	7 4 US-09-637-614-36	Sequence 59, Appl
23	70	40.0	9 1 US-08-300-386A-50	Sequence 60, Appl
23	71	40.0	9 3 US-08-931-645-50	Sequence 61, Appl
23	72	40.0	9 4 US-09-711-020A-19	Sequence 62, Appl
23	73	40.0	9 4 US-09-971-020A-21	Sequence 63, Appl
23	74	40.0	9 4 US-09-971-020A-22	Sequence 64, Appl
23	75	40.0	9 4 US-09-971-020A-22	Sequence 65, Appl
23	76	40.0	9 5 PCT-US94-0128-50	Sequence 66, Appl
23	77	40.0	9 5 PCT-US95-11235-50	Sequence 67, Appl
23	78	40.0	10 2 US-08-713-636-4	Sequence 68, Appl
23	79	40.0	10 3 US-08-213-22A-15	Sequence 69, Appl
23	80	40.0	10 5 PCT-US92-07631-16	Sequence 70, Appl
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23	83	40.0	11 1 US-08-277-660A-16	Sequence 73, Appl
23	84	40.0	11 1 US-08-424-957-28	Sequence 74, Appl
23	85	40.0	11 1 US-08-424-957-29	Sequence 75, Appl
23	86	40.0	11 1 US-08-424-957-29	Sequence 76, Appl
23	87	40.0	11 3 US-09-035-686-28	Sequence 77, Appl
23	88	40.0	11 3 US-09-035-686-29	Sequence 78, Appl
23	89	40.0	11 3 US-09-035-686-40	Sequence 79, Appl
23	90	40.0	11 3 US-09-277-660A-3	Sequence 80, Appl
23	91	40.0	11 3 US-09-424-957-33	Sequence 81, Appl
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9	29	45.0	10 3 US-09-035-686-18	Sequence 18, Appl
9	30	45.0	11 1 US-08-277-660A-9	Sequence 9, Appl
9	31	45.0	11 1 US-08-277-660A-10	Sequence 10, Appl
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9	34	45.0	11 1 US-08-277-660A-13	Sequence 13, Appl
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9	45	45.0	11 1 US-08-424-957-40	Sequence 30, Appl
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9	51	45.0	11 1 US-08-424-957-46	Sequence 36, Appl
9	52	45.0	11 1 US-08-424-957-47	Sequence 37, Appl
9	53	45.0	11 1 US-08-424-957-48	Sequence 38, Appl
9	54	45.0	11 1 US-08-424-957-49	Sequence 39, Appl
9	55	45.0	11 1 US-08-424-957-50	Sequence 40, Appl
9	56	45.0	11 1 US-08-424-957-51	Sequence 41, Appl
9	57	45.0	11 1 US-08-424-957-52	Sequence 42, Appl
9	58	43.3	5 3 US-09-035-686-34	Sequence 43, Appl
9	59	43.3	5 3 US-09-035-686-34	Sequence 44, Appl
9	60	41.7	9 1 US-08-288-405A-8	Sequence 45, Appl
9	61	41.7	11 1 US-08-424-957-44	Sequence 46, Appl
9	62	41.7	11 1 US-08-424-957-45	Sequence 47, Appl
9	63	41.7	11 1 US-08-424-957-46	Sequence 48, Appl
9	64	41.7	11 1 US-08-424-957-47	Sequence 49, Appl
9	65	41.7	11 1 US-09-035-686-46	Sequence 50, Appl
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9	68	40.0	7 4 US-09-036-749A-36	Sequence 53, Appl
9	69	40.0	7 4 US-09-637-614-36	Sequence 54, Appl
9	70	40.0	9 1 US-08-300-386A-50	Sequence 55, Appl
9	71	40.0	9 3 US-08-931-645-50	Sequence 56, Appl
9	72	40.0	9 4 US-09-711-020A-19	Sequence 57, Appl
9	73	40.0	9 4 US-09-971-020A-21	Sequence 58, Appl
9	74	40.0	9 4 US-09-971-020A-22	Sequence 59, Appl
9	75	40.0	9 5 PCT-US94-0128-50	Sequence 60, Appl
9	76	40.0	9 5 PCT-US95-11235-50	Sequence 61, Appl
9	77	40.0	9 5 PCT-US92-07631-16	Sequence 62, Appl
9	78	40.0	10 2 US-08-713-636-4	Sequence 63, Appl
9	79	40.0	10 3 US-08-213-22A-15	Sequence 64, Appl
9	80	40.0	10 5 PCT-US92-109815	Sequence 65, Appl
9	81	40.0	10 5 PCT-US92-109815	Sequence 66, Appl
9	82	40.0	11 0 US-08-277-660A-15	Sequence 67, Appl
9	83	40.0	11 1 US-08-277-660A-16	Sequence 68, Appl
9	84	40.0	11 1 US-08-424-957-28	

## ALIGNMENTS

APPLICANT: GEORGE J. DAWSON

APPLICANT: GEORGE G. SCHLAUDER

APPLICANT: SURESH M. DESAI

APPLICANT: THOMAS P. LEARY

APPLICANT: ANTHONY SCOTT MUERHOFF

APPLICANT: JAMES C. ERKER

APPLICANT: SHERI L. BUIJK

APPLICANT: ISA K. MUSHAHWAR

TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 716

CORRESPONDENCE ADDRESS:

ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

STREET: 100 ABBOTT PARK ROAD

CITY: ABBOTT PARK

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #11.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,446

FILING DATE: 2007-05-22

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/424,550

ATTORNEY/AGENT INFORMATION:

NAME: POREMBSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5527.PC.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 252:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-488-446-252

## RESULT 3

US-08-467-344A-252

Sequence 252, Application US/08467344A

; Sequence No. 6586568

; GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS

; APPLICANT: TAMI J. PILOT-MATIAS

; APPLICANT: THOMAS P. LEARY

; APPLICANT: ANTHONY SCOTT MUERHOFF

; APPLICANT: JAMES C. ERKER

; APPLICANT: SHERI L. BUIJK

; APPLICANT: ISA K. MUSHAHWAR

; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

; NUMBER OF SEQUENCES: 716

; CORRESPONDENCE ADDRESS:

RESULT 1

US-08-459-260A-252

Sequence 252, Application US/08469260A

; Patent No. 6451578

; GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS

; APPLICANT: TAMI J. PILOT-MATIAS

; APPLICANT: THOMAS P. LEARY

; APPLICANT: ANTHONY SCOTT MUERHOFF

; APPLICANT: JAMES C. ERKER

; APPLICANT: SHERI L. BUIJK

; APPLICANT: ISA K. MUSHAHWAR

; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

; NUMBER OF SEQUENCES: 716

; CORRESPONDENCE ADDRESS:

ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

STREET: 100 ABBOTT PARK ROAD

CITY: ABBOTT PARK

STATE: IL

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/424,550B

FILING DATE: 07-Jun-1995

CLASSIFICATION: 435435

ATTORNEY/AGENT INFORMATION:

NAME: POREMSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5527.PC.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 252:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 252:

US-08-467-344A-252

Query Match Score 34; DB 4; Length 8;

Best Local Similarity 85.7%; Prod. No. 4.1e+05;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 FSELWTS 11

Db 1 FSHLWTS 7

RESULT 5

US-08-424-957-5

Sequence 6, Application US/08424957

PATENT NO. 5770377

GENERAL INFORMATION:

APPLICANT: Picklesay, Steven M.

APPLICANT: Lane, David P.

APPLICANT: Interruption of Binding of MDM2 and p53

TITLE OF INVENTION: Protein and Therapeutic Application Thereof

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flier, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/424,957

FILING DATE: 19-APR-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/277,660

FILING DATE: 20-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Drager, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-61228/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1889

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

US-08-424-957-6

Query Match 50.0%; Score 30; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSBLW 9  
 Db 2 FSBLW 6

RESULT 6  
 US-09-035-686-6  
 ; Sequence 6, Application US/09035686  
 ; Patent No. 6153391  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pickley, Steven M.  
 ; ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert  
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,957  
 FILING DATE: 19-APR-1995  
 ATTORNEY / AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEX: 910 277299  
 TELEFAX: (415) 398-3249  
 INFORMATION FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 US-09-035-686-6

APPLICATION NUMBER: US 08/424,957  
 FILING DATE: 19-APR-1995  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994  
 ATTORNEY / AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEX: 910 277299  
 TELEFAX: (415) 398-3249  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 US-09-035-686-6

RESULT 8  
 US-09-035-686-42  
 ; Sequence 42, Application US/09035686  
 ; Patent No. 6153391  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pickley, Steven M.  
 ; ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/035,686  
 FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994  
 ATTORNEY / AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEX: 910 277299  
 TELEFAX: 910 277299  
 INFORMATION FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 US-08-424-957-42

Query Match 50.0%; Score 30; DB 3; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSBLW 9  
 Db 2 FSBLW 6

RESULT 7  
 US-08-424-957-42  
 ; Sequence 42, Application US/08424957  
 ; Patent No. 5770377  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pickley, Steven M.  
 ; ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/035,686  
 FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:



TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19  
 OTHER INFORMATION: binding polypeptide  
 US-09-669-271A-6

Qy	Db	4 FFSELMNTS 11	1 FFCALWPS 8
RESULT 13			
US-09-881-276-6			
; Sequence 6, Application US/09881276			
; Patent No. 6479641			
; GENERAL INFORMATION:			
; APPLICANT: Whelihan, E. Favelle			
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19			
; FILE REFERENCE: DYX-009.0 US-2			
; CURRENT APPLICATION NUMBER: US/09/881,276			
; CURRENT FILING DATE: 2001-06-14			
; PRIOR APPLICATION NUMBER: 09/669,271			
; PRIOR FILING DATE: 2000-09-26			
; PRIOR APPLICATION NUMBER: 09/186,958			
; NUMBER OF SEQ ID NOS: 27			
; SOFTWARE: Microsoft Word 97			
; SEQ ID NO: 6			
; LENGTH: 11			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide			
; US-09-881-276-6			
Query Match 46.7%; Score 28; DB 4; Length 11;			
Best Local Similarity 62.5%; Pred. No. 1.2e+02; Mismatches 5; Conservative 0; Indels 0; Gaps 0;			
Matches 5; Mismatches 3; Indels 0; Gaps 0;			
RESULT 14			
US-08-277-660A-2			
; Sequence 2, Application US/08277660A			
; Patent No. 5702908			
; GENERAL INFORMATION:			
; APPLICANT: Picklesley, Steven M.			
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53			
; NUMBER OF SEQUENCES: 50			
; CORRESPONDENCE ADDRESS:			
; ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert			
; STREET: Four Embarcadero Center, Suite 3400			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: United States			
; ZIP: 94111-4187			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US 08/277,660			
; FILING DATE: 20-JUL-1994			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Dreger, Walter H.			
; REGISTRATION NUMBER: 24,190			
; REFERENCE/DOCKET NUMBER: A-61228/WHD			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 781-1989			
; TELEFAX: (415) 398-3249			
; TELEX: 910 277299			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 6 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: unknown			
; TOPOLOGY: linear			
US-08-277-660A-2			
Query Match 45.0%; Score 27; DB 1; Length 6;			
Best Local Similarity 80.0%; Pred. No. 4.1e+05; Mismatches 0; Indels 0; Gaps 0;			
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
RESULT 15			
US-08-424-957-2			
; Sequence 2, Application US/08424957			
; Patent No. 5770377			
; GENERAL INFORMATION:			
; APPLICANT: Lane, David P.			
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof			
; NUMBER OF SEQUENCES: 50			
; CORRESPONDENCE ADDRESS:			
; ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert			
; STREET: Four Embarcadero Center, Suite 3400			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: United States			
; ZIP: 94111-4187			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US 08/424,957			
; FILING DATE: 19-APR-1995			
; CLASSIFICATION:			
; PRIORITY APPLICATION DATA:			
; APPLICATION NUMBER: US 08/277,660			
; FILING DATE: 20-JUL-1994			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Dreger, Walter H.			
; REGISTRATION NUMBER: 24,190			
; REFERENCE/DOCKET NUMBER: A-61228/WHD			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 781-1989			
; TELEFAX: (415) 398-3249			
; TELEX: 910 277299			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 6 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: unknown			
; TOPOLOGY: unknown			
US-08-424-957-2			

Query Match 45.0%; Score 27; DB 1; Length 6;

APPLICATION NUMBER: US/08/277,660

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/424-957-2

, Thu Aug 4 07:03:40 2005

Best Local Similarity 80.0%; Pred. No. 4.1e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 1;

QY	5	FSELW	9
Db	2	FSDW	6

Search completed: August 3, 2005, 18:42:34  
Job time : 48 sec<sub>B</sub>

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## Om protein - protein search, using sw model

Run on: August 3, 2005, 18:41:15 ; Search time 154 Seconds

(without alignments)  
27.829 Million cell updates/sec

Title: US-10-088-681-1

Perfect score: 60

Sequence: 1 TGSFFSELWTS 11

Scoring table: BIOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 227232

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 100%

Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA:<sup>\*</sup>

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6:	/cgn2_6/ptodata/2/pubpaa/PCTNS_PUBCOMB.pep:*	17	45.0	6	15	US-10-666-698-130	Sequence 130, App
7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*	18	45.0	6	15	US-10-683-045-130	Sequence 130, App
8:	/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*	19	45.0	6	18	US-10-694-276A-83	Sequence 130, App
9:	/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*	20	45.0	6	18	US-10-97-262A-38	Sequence 83, Appli
10:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*	21	45.0	6	18	US-10-97-262A-38	Sequence 2, Appli
11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*	22	45.0	8	16	US-10-940-179-2	Sequence 3, Appli
12:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*	23	45.0	8	16	US-10-940-179-3	Sequence 37, Appli
13:	/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*	24	45.0	9	9	US-09-214-371-37	Sequence 38, Appli
14:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*	25	45.0	9	9	US-09-214-371-38	Sequence 1, Appli
15:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*	26	45.0	9	16	US-10-940-179-1	Sequence 37, Appli
16:	/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*	27	45.0	9	18	US-10-957-262A-37	Sequence 38, Appli
17:	/cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*	28	45.0	9	18	US-10-97-262A-38	Sequence 39, Appli
18:	/cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep:*	29	45.0	10	17	US-10-726-322-107	Sequence 36, Appli
19:	/cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*	30	45.0	11	11	US-09-840-085-31	Sequence 31, Appli
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22:	/cgn2_6/ptodata/2/pubpaa/US11E_PUBCOMB.pep:*	33	45.0	11	15	US-10-987-957-38	Sequence 38, Appli
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		35	45.0	11	15	US-10-987-957-39	Sequence 36, Appli
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		44	45.0	11	16	US-10-931-722-3	Sequence 37, Appli
		45	45.0	11	16	US-10-488-219-37	Sequence 38, Appli
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		48	45.0	11	16	US-10-601-953-812	Sequence 812, App
		49	45.0	11	16	US-10-222-265-708	Sequence 70B, App
		50	45.0	11	16	US-10-631-722-3	Sequence 3, Appli
		51	45.0	11	16	US-10-488-955-233	Sequence 233, App
		52	45.0	11	16	US-10-488-955-235	Sequence 39, App
		53	45.0	11	16	US-10-462-452-707	Sequence 237, App
		54	45.0	11	16	US-10-480-954-239	Sequence 239, App
		55	45.0	11	16	US-10-450-036A-14	Sequence 245, App
		56	45.0	11	16	US-10-190-193-180	Sequence 180, App
		57	45.0	11	16	US-10-239-656-11	Sequence 11, Appli
		58	45.0	11	16	US-10-893-576-86	Sequence 235, App
		59	45.0	11	16	US-10-480-954-237	Sequence 237, App
		60	45.0	11	16	US-10-480-954-239	Sequence 239, App
		61	45.0	11	16	US-10-450-036A-14	Sequence 245, App
		62	45.0	11	16	US-10-327-598-457	Sequence 457, App
		63	45.0	11	16	US-10-725-962-62	Sequence 62, Appli
		64	45.0	11	16	US-10-725-962-65	Sequence 66, Appli
		65	45.0	11	16	US-10-031-874-14	Sequence 14, Appli
		66	45.0	11	16	US-10-631-611-5	Sequence 5, Appli
		67	45.0	11	16	US-10-450-036A-14	Sequence 14, Appli
		68	45.0	11	16	US-10-327-598-457	Sequence 457, App
		69	45.0	11	16	US-10-190-082-171	Sequence 171, Appli
		70	45.0	11	16	US-10-190-082-170	Sequence 290, App
		71	45.0	11	16	US-10-097-175-60	Sequence 60, Appli
		72	45.0	11	16	US-10-098-187-581	Sequence 59, Appli
		73	45.0	11	16	US-10-221-022-3	Sequence 3, Appli
		74	45.0	11	16	US-09-056-7493-36	Sequence 36, Appli
		75	45.0	11	16	US-10-903-412-36	Sequence 36, Appli
		76	45.0	11	16	US-10-174-717A-36	Sequence 36, Appli
		77	45.0	11	16	US-10-165-155-36	Sequence 36, Appli
		78	45.0	11	16	US-10-190-162-36	Sequence 5, Appli
		79	45.0	11	16	US-10-480-954-51	Sequence 36, Appli
		80	45.0	11	16	US-10-480-954-53	Sequence 51, Appli
		81	45.0	11	16	US-10-480-954-55	Sequence 55, Appli
		82	45.0	11	16	US-10-480-954-119	Sequence 119, Appli
		83	45.0	11	16	US-10-480-954-121	Sequence 121, Appli
		84	45.0	11	16	US-10-480-954-123	Sequence 123, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length DB ID	Description
1	34	56.7	8 US-09-424-550B-252 Sequence 252, Appli
2	30	50.0	10 9 US-09-214-371-35 Sequence 35, Appli
3	30	50.0	10 9 US-09-214-371-36 Sequence 36, Appli
4	30	50.0	10 18 US-10-927-262A-35 Sequence 35, Appli
5	30	50.0	10 18 US-10-927-262A-36 Sequence 36, Appli
6	29	48.3	7 16 US-10-888-271-10 Sequence 10, Appli
7	29	48.3	10 17 US-10-659-201-28 Sequence 28, Appli
8	28	46.7	9 9 US-09-486-734A-35 Sequence 35, Appli
9	28	46.7	11 9 US-09-881-276-6 Sequence 6, Appli
10	28	46.7	11 15 US-10-417-895A-56 Sequence 56, Appli
11	27	45.0	9 US-09-214-371-83 Sequence 83, Appli

RESULT 1  
US-08-24-550B-252  
; Publication No. US2002011947A1  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUERHOPF  
APPLICANT: JAMES C. ECKER  
APPLICANT: SHERI L. BIJUK  
APPLICANT: ISA K. MUSHARHAW  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OR INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716

CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
MEDIUM TYPE: FLOPPY disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
CLASSIFICATION: 431435  
ATTORNEY/AGENT INFORMATION:  
NAME: POREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 252:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
MOLECULE TYPE: protein

US-08-424-550B-252

Query Match 55.7%; Score 34; DB 8; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.6e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 2  
US-09-214-371-35  
; Sequence 35, Application US/09214371B  
; Patent No. US2001018511A1  
GENERAL INFORMATION:  
APPLICANT: Lane, David  
APPLICANT: Bottger, Volker  
APPLICANT: Bottger, Angelica  
APPLICANT: Picklsey, Stephen  
APPLICANT: Chen, Patrick  
APPLICANT: Hochkeppel, Heinz-Kurt  
APPLICANT: Garcia-Echeverria, Carlos  
APPLICANT: Forlet, Pascal  
TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2  
FILE REFERENCE: 4-20937/A/PCT  
CURRENT APPLICATION NUMBER: US/09/214,371B  
CURRENT FILING DATE: 1999-03-26  
PRIORITY APPLICATION NUMBER: PCT/EP97/03549  
PRIOR FILING DATE: 1997-07-04  
NUMBER OF SEQ ID NOS: 83  
SEQ ID NO 35

Qy 2 GSFSEELW 9  
Db 2 GPFPSDLW 9

RESULT 3  
US-09-214-371-36  
; Sequence 36, Application US/09214371B  
; Patent No. US2001018511A1  
GENERAL INFORMATION:  
APPLICANT: Lane, David  
APPLICANT: Bottger, Volker  
APPLICANT: Bottger, Angelica  
APPLICANT: Picklsey, Stephen  
APPLICANT: Chen, Patrick  
APPLICANT: Hochkeppel, Heinz-Kurt  
APPLICANT: Garcia-Echeverria, Carlos  
APPLICANT: Forlet, Pascal  
TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2  
FILE REFERENCE: 4-20937/A/PCT  
CURRENT APPLICATION NUMBER: US/09/214,371B  
CURRENT FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: PCT/EP97/03549  
PRIOR FILING DATE: 1997-07-04  
NUMBER OF SEQ ID NOS: 83  
SEQ ID NO 36

LENGTH: 10

Qy 5 FSEIWTs 11  
Db 1 FSHLWtS 7

ALIGNMENTS

TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
; NAME/KEY: VARIANT  
; LOCATION: (1)  
; OTHER INFORMATION: X = Ac-CYS  
; NAME/KEY: VARIANT  
; LOCATION: (0)  
; OTHER INFORMATION: x = Pro-NH2

US-09-214-371-36

Query Match 50.0%; Score 30; DB 9; Length 10;  
; Best Local Similarity 62.5%; Pred. No. 1.9e+02;  
; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSFFSELMW 9  
Db 2 GPTFSDLW 9

RESULT 4

US-10-97-262A-35

; Sequence 35, Application US/10927262A  
; Publication No. US20050137137A1  
; GENERAL INFORMATION:  
; APPLICANT: LANE, DAVID P  
; APPLICANT: BOTTLER, VOLKER  
; APPLICANT: BOTTLER, ANGELIKA  
; APPLICANT: PIKSLER, STEVEN M  
; APPLICANT: HOCHKEPPEL, HEINZ-KURT  
; APPLICANT: GARCIA-ECHEVERRIA, CARLOS  
; APPLICANT: CHENE, PATRICK  
; APPLICANT: FORET, PASCAL

TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2  
FILE REFERENCE: 39749.0002 AIC CON  
CURRENT APPLICATION NUMBER: US/10/927.262A  
CURRENT FILING DATE: 2004-08-25  
PRIOR APPLICATION NUMBER: 09/214,371  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: PCT/EP97/03549  
PRIOR FILING DATE: 1997-07-04  
PRIOR APPLICATION NUMBER: GB 9614197.3  
PRIOR FILING DATE: 1996-07-05  
PRIOR APPLICATION NUMBER: GB 9707041.1  
PRIOR FILING DATE: 1997-04-07  
PRIOR APPLICATION NUMBER: PCT/EP97/03549  
PRIOR FILING DATE: 1997-07-04  
PRIOR APPLICATION NUMBER: GB 9614197.3  
PRIOR FILING DATE: 1996-07-05  
PRIOR APPLICATION NUMBER: GB 9707041.1  
PRIOR FILING DATE: 1997-04-07  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 35  
LENGTH: 10

RESULT 5

US-10-927-262A-36

Query Match 50.0%; Score 30; DB 18; Length 10;  
; Best Local Similarity 62.5%; Pred. No. 1.9e+02;  
; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSFFSELMW 9  
Db 2 GPTFSDLW 9

RESULT 6

US-10-858-271-10

; Sequence 10, Application US/10858271  
; Publication No. US20040259829A1  
; GENERAL INFORMATION:  
; APPLICANT: Danks, Mary K  
; APPLICANT: Porter, Philip M.  
; APPLICANT: Houghton, Peter J.  
; APPLICANT: Dahms, Mary K.  
; APPLICANT: Porter, Philip M.  
; TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of Tumor Cells  
FILE REFERENCE: SJ-0005  
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of Tumor Cells  
CURRENT APPLICATION NUMBER: US/10/858.271  
CURRENT FILING DATE: 2004-06-01  
PRIOR APPLICATION NUMBER: US/09/595,682  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/075,258  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: PCT/US99/03171  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 30  
SEQ ID NO 10  
LENGTH: 7

Query Match 48.3%; Score 29; DB 16; Length 7;  
; Best Local Similarity 57.1%; Pred. No. 1.6e+06;  
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GSFFSELMW 9  
Db 2 GPTFSDLW 9

RESULT 5

US-10-927-262A-36

; Sequence 36, Application US/10927262A

Query Match 48.3%; Score 29; DB 16; Length 7;  
; Best Local Similarity 57.1%; Pred. No. 1.6e+06;  
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

US-10-858-271-10

Query Match 48.3%; Score 29; DB 16; Length 7;  
; Best Local Similarity 57.1%; Pred. No. 1.6e+06;  
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Publication No. US20050137137A1  
; GENERAL INFORMATION:  
; APPLICANT: LANE, DAVID P  
; APPLICANT: BOTTLER, VOLKER  
; APPLICANT: BOTTLER, ANGELIKA  
; APPLICANT: PIKSLER, STEVEN M.  
; APPLICANT: HOCHKEPPEL, HEINZ-KURT  
; APPLICANT: GARCIA-ECHEVERRIA, CARLOS  
; APPLICANT: CHENE, PATRICK  
; APPLICANT: FORET, PASCAL  
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2  
; FILE REFERENCE: 39749.0002 AIC CON  
; CURRENT APPLICATION NUMBER: US/10/927.262A  
; CURRENT FILING DATE: 2004-08-25  
; PRIOR APPLICATION NUMBER: 09/214,371  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-04-07  
; NUMBER OF SEQ ID NOS: 85  
; SEQ ID NO 36  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide

US-10-927-262A-36

Query Match 50.0%; Score 30; DB 18; Length 10;  
; Best Local Similarity 62.5%; Pred. No. 1.9e+02;  
; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSFFSELMW 9  
Db 2 GPTFSDLW 9

RESULT 6

US-10-858-271-10

; Sequence 10, Application US/10858271  
; Publication No. US20040259829A1  
; GENERAL INFORMATION:  
; APPLICANT: Danks, Mary K  
; APPLICANT: Porter, Philip M.  
; APPLICANT: Houghton, Peter J.  
; APPLICANT: Dahms, Mary K.  
; APPLICANT: Porter, Philip M.  
; TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of Tumor Cells  
FILE REFERENCE: SJ-0005  
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of Tumor Cells  
CURRENT APPLICATION NUMBER: US/10/858.271  
CURRENT FILING DATE: 2004-06-01  
PRIOR APPLICATION NUMBER: US/09/595,682  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/075,258  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: PCT/US99/03171  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 30  
SEQ ID NO 10  
LENGTH: 7

Query Match 48.3%; Score 29; DB 16; Length 7;  
; Best Local Similarity 57.1%; Pred. No. 1.6e+06;  
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

US-10-858-271-10

Query Match 48.3%; Score 29; DB 16; Length 7;  
; Best Local Similarity 57.1%; Pred. No. 1.6e+06;  
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Publication No. US20050137137A1  
; GENERAL INFORMATION:  
; APPLICANT: LANE, DAVID P  
; APPLICANT: BOTTLER, VOLKER  
; APPLICANT: BOTTLER, ANGELIKA  
; APPLICANT: PIKSLER, STEVEN M.  
; APPLICANT: HOCHKEPPEL, HEINZ-KURT  
; APPLICANT: GARCIA-ECHEVERRIA, CARLOS  
; APPLICANT: CHENE, PATRICK  
; APPLICANT: FORET, PASCAL  
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2  
; FILE REFERENCE: 39749.0002 AIC CON  
; CURRENT APPLICATION NUMBER: US/10/927.262A  
; CURRENT FILING DATE: 2004-08-25  
; PRIOR APPLICATION NUMBER: 09/214,371  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-04-07  
; NUMBER OF SEQ ID NOS: 85  
; SEQ ID NO 36  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Oryctolagus cuniculus

US-10-858-271-10

Query Match 48.3%; Score 29; DB 16; Length 7;  
; Best Local Similarity 57.1%; Pred. No. 1.6e+06;  
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

US-10-858-271-10

Query Match 48.3%; Score 29; DB 16; Length 7;  
; Best Local Similarity 57.1%; Pred. No. 1.6e+06;  
; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy            3 SFFSELW 9  
               :|:|||  
               1 AFTTELW 7

RESULT 7  
 US-10-659-207-28  
 ; Sequence 28, Application US/10659207  
 ; Publication No. US2005003795A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CWRILA, STEVEN E.  
 ; APPLICANT: DUFFIN, DAVID J.  
 ; APPLICANT: MIRILLI, SUNILIA  
 ; APPLICANT: SCHALTZ, PETER JOSEPH  
 ; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY  
 ; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSPR) AND ASSOCIATED  
 ; TITLE OF INVENTION: USES  
 ; FILE REFERENCE: 0300-0014  
 ; CURRENT APPLICATION NUMBER: US/10/659, 207  
 ; CURRENT FILING DATE: 2003-09-09  
 ; PRIOR APPLICATION NUMBER: US/09/620, 091  
 ; PRIOR FILING DATE: 2000-07-20  
 ; NUMBER OF SEQ ID NOS: 491  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 28  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: peptide  
 ; US-10-659-207-28

Query Match      Best Local Similarity 48.3%; Score 29; DB 17; Length 10;  
                   Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	3 SFFSELW 9	Db	3 SFFSELW 9
	:		

RESULT 8  
 US-09-886-734A-35  
 ; Sequence 35, Application US/09486734A  
 ; Patient No. US2002016473A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chopin, Marie-Christine  
 ; APPLICANT: Clerc, Florence  
 ; APPLICANT: Erlich, S. Busko  
 ; APPLICANT: Gautier, Michel  
 ; APPLICANT: Schouler, Catherine  
 ; APPLICANT: Institut National de la Recherche Agronomique  
 ; TITLE OF INVENTION: Resistance Mechanisms to IC Type R/M  
 ; TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria  
 ; FILE REFERENCE: 33339/156048  
 ; CURRENT APPLICATION NUMBER: US/09/486, 734A  
 ; CURRENT FILING DATE: 2000-05-03  
 ; PRIOR APPLICATION NUMBER: PCT/FR98/01873  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: FR 97/10885  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 35  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: variant peptide for third complementarity  
 ; OTHER INFORMATION: determining region of Fv region of an  
 ; OTHER INFORMATION: immunoglobulin  
 ; US-09-486-734A-35

Query Match      Best Local Similarity 46.7%; Score 28; DB 15; Length 11;  
                   Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy	3 SFFSELWTS 11	Db	2 GSFPKQL 8
	:    :		

RESULT 9  
 US-09-881-276-6  
 ; Sequence 6, Application US/09881276  
 ; Patent No. US20020031761A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wheilhan, E. Fayelle  
 ; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19  
 ; FILE REFERENCE: DXY-009-0 US-2  
 ; CURRENT APPLICATION NUMBER: US/09/881, 276  
 ; CURRENT FILING DATE: 2001-06-14  
 ; PRIOR APPLICATION NUMBER: 09/1669, 271  
 ; PRIOR FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: 09/1186, 958  
 ; PRIOR FILING DATE: 1998-11-05  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: Microsoft Word 97  
 ; SEQ ID NO 6  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide  
 ; OTHER INFORMATION: peptide  
 ; US-09-881-276-6

Query Match      Best Local Similarity 46.7%; Score 28; DB 9; Length 11;  
                   Matches 5; Conservative 62.5%; Mismatches 0; Indels 0; Gaps 0;

Qy	4 FFSELWTS 11	Db	1 FFCALWPS 8
	:		

RESULT 10  
 US-10-17-895A-56  
 ; Sequence 56, Application US/10417895A  
 ; Publication No. US20040033569A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Crea, Roberto  
 ; APPLICANT: Cappuccilli, Guido  
 ; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS  
 ; FILE REFERENCE: 1551.2002-001  
 ; CURRENT APPLICATION NUMBER: US/10/417, 895A  
 ; CURRENT FILING DATE: 2003-04-16  
 ; PRIOR APPLICATION NUMBER: 60/373, 686  
 ; PRIOR FILING DATE: 2002-04-17  
 ; NUMBER OF SEQ ID NOS: 86  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 56  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: variant peptide for third complementarity  
 ; OTHER INFORMATION: determining region of Fv region of an  
 ; OTHER INFORMATION: immunoglobulin  
 ; US-10-17-895A-56

Query Match      Best Local Similarity 44.4%; Score 28; DB 15; Length 11;  
                   Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy	3 SFFSELWTS 11	Db	2 GSFPKQL 8
	:    :		

Db 1 | :| | :| SYSSSWSS 9

RESULT 11  
US-09-214-371-83  
; Sequence 83, Application US/09214371B  
; Patent No. US2001001851A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Picklesley, Stephen  
; APPLICANT: Chane, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2  
; FILE REFERENCE: 4-20931/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 83  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide, amin  
; OTHER INFORMATION: acid residues 18-23 of human p53  
US-09-214-371-83

Query Match Best Local Similarity 45.0%; Score 27; DB 9; Length 6;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSELW 9  
Db 2 PSDLW 6

---

RESULT 12  
US-09-732-384-4  
; Sequence 4, Application US/09732384  
; Patent No. US2002012977A1  
; GENERAL INFORMATION:  
; APPLICANT: Yuan, Zhi-Min  
; APPLICANT: Gu, Jie-Jie  
; TITLE OF INVENTION: Inhibition of p53 Degradation  
; FILE REFERENCE: 21508-044  
; CURRENT APPLICATION NUMBER: US/09/732,384  
; CURRENT FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: 60/169,816  
; PRIOR FILING DATE: 1999-12-08  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; OTHER INFORMATION: Description of Artificial Sequence:Protein  
; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide  
US-09-732-384-4

Query Match Best Local Similarity 45.0%; Score 27; DB 9; Length 6;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSELW 9  
Db 2 PSDLW 6

---

RESULT 13  
US-10-155-059-1  
; Sequence 1, Application US/10155059  
; Publication No. US20020147173A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; APPLICANT: Jost, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
; ANTIBODIES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon Peabody LLP  
; STREET: 101 Federal Street  
; CITY: Boston  
; STATE: MA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/155,059  
; FILING DATE: 24-MAY-2002  
; CLASSIFICATION: <Unknown>  
; PRIORITY/AGENT INFORMATION:  
; NAME: Eisenstein, Ronald I  
; REGISTRATION NUMBER: 30,628  
; REFERENCE/DOCKET NUMBER: 47400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-6054  
; TELEFAX: 617-345-1300  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-155-059-1

Query Match Best Local Similarity 45.0%; Score 27; DB 13; Length 6;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSELW 9  
Db 2 PSDLW 6

---

RESULT 14  
US-10-609-217-130  
; Sequence 130, Application US/10609217  
; Publication No. US2004004188A1  
; GENERAL INFORMATION:  
; APPLICANT: FELGB, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-227  
; CURRENT APPLICATION NUMBER: US/10/609,217

Query Match Best Local Similarity 80.0%; Score 27; DB 9; Length 6;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSELW 9  
Db 2 PSDLW 6

; CURRENT FILING DATE: 2003-05-27  
 ; PRIOR APPLICATION NUMBER: US/09/428,082B  
 ; PRIOR FILING DATE: 1999-10-22  
 ; PRIOR APPLICATION NUMBER: 60/105,371  
 ; NUMBER OF SEQ ID NOS: 1133  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 130  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE  
 ; US-10-609-217-130  
 Query Match Score 27; DB 15; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.6e+06;  
 Matches 4; Conservatve 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 FSLIW 9  
 Db 2 FSLIW 6

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RESULT 15  
 US-10-632-388-130  
 ; Sequence 130, Application US/10632388  
 ; Publication No. US20040053845A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FEIGE, ULRICH  
 ; APPLICANT: LIU, CHUAN-FA  
 ; APPLICANT: CREETHAM, JANET C.  
 ; APPLICANT: BOONE, THOMAS CHARLES  
 ; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
 ; FILE REFERENCE: A-527  
 ; CURRENT APPLICATION NUMBER: US/10/632,388  
 ; CURRENT FILING DATE: 2003-07-31  
 ; PRIOR APPLICATION NUMBER: US/09/428,082B  
 ; PRIOR FILING DATE: 1999-10-22  
 ; PRIOR APPLICATION NUMBER: 60/105,371  
 ; PRIOR FILING DATE: 1998-10-23  
 ; NUMBER OF SEQ ID NOS: 1133  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 130  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE  
 ; US-10-632-388-130

Query Match	45.0%	Score	27	DB	15	Length	6
Best Local Similarity	80.0%	Pred. No.	1.6e+06				
Matches	4	Conservative	1	Mismatches	0	Indels	0
Qy	5	FSLIW	9				
Db	2	FSLIW	6				

Search completed: August 3, 2005, 18:54:35  
 Job time : 162 secs



## ALIGNMENTS

RESULT 1			
C39191	hypothetical protein 1 (Tetx 5' region) - <i>Bacteroides fragilis</i>		
C;Species: <i>Bacteroides fragilis</i>			
C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993			
R;Speer, B.S.; Bedzyk, L.; Salvers, A.A.			
J; Bacteriol. 173, 176-183, 1991			
A;Title: Evidence that a novel tetracycline resistance gene found on two <i>Bacteroides</i> tra			
A;Reference number: A39191; MUID:91100280; PMID:1846135			
A;Accession: C39191			
A;Status: preliminary; not compared with conceptual translation			
A;Molecule type: DNA			
A;Residues: 1-10 <SPE>			
A;Cross-references: GB:M37699			
Query Match	Score 30; DB 2; Length 10;		
Best Local Similarity 62.5%; Pred. No. 32; Mismatches 1; Indels 0; Gaps 0;			
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
Qy 5 FRSBLWTS 12			
Db 2 YFSRPWTS 9			
RESULT 2			
S36850	Ig heavy chain V region - mouse		
C;Species: <i>Mus musculus</i> (house mouse)			
C;Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999			
C;Accession: S36850			
R;Jacob, J.; Kelsoe, G.			
R;Submitted to the EMBL Data Library, July 1992			
A;Description: In situ studies on the primary immune response to 4-hydroxy-3-nitrophenyl			
A;Reference number: S25024			
A;Accession: S36850			
A;Status: preliminary			
A;Molecule type: nucleic acid			
A;Residues: 1-9 <JAC>			
A;Cross-references: EMBL:X07387; NID:950113; PIDN:CAA47799.1; PID:e51594; PID:91333871			
C;Keywords: heterotetramer; immunoglobulin			
Query Match	Score 28; DB 2; Length 9;		
Best Local Similarity 66.7%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;			
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 EVGSFFP 6			
Db 4 DYGSYF 9			
RESULT 3			
PT0274	Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)		
C;Species: <i>Homo sapiens</i> (man)			
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996			
C;Accession: PT0274			
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.			
J; Exp. Med. 173, 395-407, 1991			
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and			
A;Reference number: PT0222; MUID:9108337; PMID:1899102			
A;Accession: PT0274			
A;Molecule type: DNA			
A;Residues: 1-12 <YAM>			
A;Experimental source: B lymphocyte			
C;Keywords: heterotetramer; immunoglobulin			
Query Match	Score 25; DB 2; Length 12;		
Best Local Similarity 57.1%; Pred. No. 2.9e+02; Mismatches 1; Indels 0; Gaps 0;			
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
RESULT 4			
PH1602	Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)		
C;Species: <i>Mus musculus</i> (house mouse)			
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999			
C;Accession: PH1602			
R;Lwinson, D.A.; Campos-Torres, J.; Leder, P.			
J; Exp. Med. 178, 317-329, 1993			
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice			
A;Reference number: PH1580; MUID:93301609; PMID:8315387			
A;Accession: PH1602			
A;Molecule type: DNA			
A;Residues: 1-7 <LEV>			
A;Experimental source: bone marrow pre-B lymphocyte			
C;Keywords: immunoglobulin			
Query Match	Score 24; DB 2; Length 7;		
Best Local Similarity 80.0%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;			
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy 7 SELWLT 11			
Db 3 SSLWLT 7			
RESULT 5			
G41946	T-cell receptor gamma chain (2t-23) - mouse (fragment)		
C;Species: <i>Mus musculus</i> (house mouse)			
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999			
C;Accession: G41946			
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.			
Mol. Cell. Biol. 11, 5930-5909, 1991			
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ger			
A;Reference number: A41946; MUID:92049316; PMID:1658619			
A;Accession: G41946			
A;Status: preliminary; not compared with conceptual translation			
A;Molecule type: DNA			
A;Residues: 1-9 <WHE>			
C;Keywords: T-cell receptor			
Query Match	Score 22; DB 2; Length 9;		
Best Local Similarity 66.7%; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;			
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
Qy 2 YGSFFPS 7			
Db 2 YGSYSS 7			
RESULT 6			
B34835	dnab protein - <i>Pseudomonas aeruginosa</i> (fragment)		
C;Species: <i>Pseudomonas aeruginosa</i>			
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999			
C;Accession: B34835			
R;Yee, T.W.; Smith, D.W.			
Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990			
A;Title: Pseudomonas chromosome replication origins: a bacterial class distinct from Es			
A;Reference number: A34835; MUID:90160310; PMID:2106132			
A;Accession: B34835			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-6 <YEE>			
A;Cross-references: GB:M30125; NID:9151419; PIDN:AAA25916.1; PID:9151421			
C;Keywords: DNA binding			

Query Match	29.9%;	Score 20;	DB 2;	Length 6;	
Best Local Similarity	100.0%;	Pred. No.	2.8e+05;		
Matches	3;	Conservative	0;	Mismatches	0;
Qy	8	ELW 10		Indels	0;
Db	4	ELW 6		Gaps	0;
RESULT 7					
C.Species:	mitochondrion Bipes biporus				
C.Accession:	T13838				
C.Date:	20-Sep-1999	#sequence_revision	20-Sep-1999	#text_change	09-Jul-2004
A.Title:	Two novel gene orders and the role of light-strand replication in rearrangement				
A.Reference number:	Z17789; MUID:91753232; PMID:1000757				
A.Accession:	T13838				
A.Status:	preliminary; translated from GB/EMBL/DDJB				
A.Molecule type:	DNA				
A.Residues:	1-10 <MAC>				
A.Cross-references:	UNIPROT:P92576; EMBL:U71335; NID:91753232; PID:91753235; PIDN:AAB482				
A.Genome:	mitochondrion				
A.Note:	COL				
A;Keywords:	mitochondrion; oxidoreductase				
Query Match	29.9%;	Score 20;	DB 2;	Length 10;	
Best Local Similarity	100.0%;	Pred. No.	1.8e+03;		
Matches	4	SFFS 7			
Qy					
Db	6	SFFS 9			
RESULT 8					
C.Species:	Periplaneta americana (American cockroach)				
C.Accession:	S05002				
C.Date:	07-Sep-1990	#sequence_revision	09-Apr-1998	#text_change	09-Jul-2004
A.Title:	Isolation and structure of corazonin, a cardioactive peptide from the american				
A.Reference number:	S05002; MUID:89325572; PMID:2753132				
A.Accession:	S05002				
A.Molecule type:	protein				
A.Residues:	1-11 <VEE>				
A;Cross-references:	UNIPROT:P11496				
A;Keywords:	amidated carboxyl end; neuropeptide; pyroglutamic acid (Gln) #stataus experimental				
F11/Modified site:	pyrrolidone carboxylic acid (Gln) #stataus experimental				
Query Match	29.9%;	Score 20;	DB 2;	Length 11;	
Best Local Similarity	42.9%;	Pred. No.	2e+03;		
Matches	3;	Conservative	2;	Mismatches	2;
Qy	6	FSELWTS 12		Indels	0;
Db	5	YSRGWTN 11		Gaps	0;
RESULT 9					
C.Species:	Mytilus edulis (blue mussel)				
C.Accession:	B61445				
C.Date:	07-Oct-1994	#sequence_revision	07-Oct-1994	#text_change	21-Jan-2000
A.Title:	Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis				
A.Reference number:	A61445; MUID:84144823; PMID:6583690				
A;Keywords:	neuropeptide; pedal ganglia				
C;Keywords:	neuropeptide; opioid peptide				
Query Match	28.4%;	Score 19;	DB 2;	Length 5;	
Best Local Similarity	75.0%;	Pred. No.	2.8e+05;		
Matches	3;	Conservative	0;	Mismatches	1;
Qy	2	YGSF 5		Indels	0;
Db	1	YGGF 4		Gaps	0;
RESULT 10					
C.Species:	Mytilus edulis (blue mussel)				
C.Date:	07-Oct-1994	#sequence_revision	07-Oct-1994	#text_change	21-Jan-2000
C.Accession:	A61445				
R;Leung, M.K.; Stefano, G.B.					
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984					
A;Title:	Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis				
A;Reference number:	A61445; MUID:84144823; PMID:6583690				
A;Accession:	A61445				
A;Molecule type:	protein				
A;Residues:	1-5 <LEU>				
A;Experimental source:	pedal ganglia				
C;Keywords:	neuropeptide; opioid peptide				
Query Match	28.4%;	Score 19;	DB 2;	Length 5;	
Best Local Similarity	75.0%;	Pred. No.	2.8e+05;		
Matches	3;	Conservative	0;	Mismatches	1;
Qy	2	YGSF 5		Indels	0;
Db	1	YGGF 4		Gaps	0;
RESULT 11					
PT0519					
T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)					
C.Species:	Mus musculus (house mouse)				
C.Date:	17-Jul-1992	#sequence_revision	17-Jul-1992	#text_change	30-May-1997
C;Accession:	PT0519				
R;Feeney, A.J.					
J. Exp. Med. 174, 115-124, 1991					
A;Title:	Junctional sequences of fetal T cell receptor beta chains have few N regions				
A;Reference number:	PT0509; MUID:91277601; PMID:1711558				
A;Accession:	PT0519				
A;Status:	transplantation not shown				
A;Molecule type:	mRNA				
A;Residues:	1-6 <FEE>				
A;Experimental source:	adult thymus, strain BALB/C				
C;Keywords:	T-cell receptor				
Query Match	28.4%;	Score 19;	DB 2;	Length 6;	
Best Local Similarity	75.0%;	Pred. No.	2.8e+05;		
Matches	3;	Conservative	0;	Mismatches	1;
Qy	7	SSIW 10		Indels	0;
Db	2	SSIW 5		Gaps	0;
RESULT 12					
A43129					
neuropeptide GNPFPRamide - tapeworm (Moniezia expansa)					
C.Species:	Moniezia expansa				
C.Date:	10-Nov-1997	#sequence_revision	14-Nov-1997	#text_change	09-Jul-2004

C;Accession: A43129  
 R;Maule, A.; Shaw, C.; Halton, D.; Thim, L.  
 Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993  
 A;Title: GNRFRamide: A novel FMRFamide-immunoactive peptide isolated from the sheep pituitary gland  
 A;Reference number: A43129; MUID:93312289; PMID:8323531  
 A;Accession: A43129  
 A;Molecule type: protein  
 A;Residues: 1-6 <MAU>  
 A;Cross-references: UNIPROT:P41966  
 C;Keywords: amidated carboxyl end; neuropeptide  
 F;6/Modified site: amidated carboxyl end (phe) #status predicted

Query Match 28.4%; Score 19; DB 2; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	3	GSFF 6	
Db	1	GNFF 4	

RESULT 13

A60224  
 Met-enkephalin-Arg-Phe - rabbit  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Accession: A60224  
 C;Date: 21-Oct-1992 #sequence\_revision 21-Oct-1992 #text\_change 02-Sep-2000  
 R;Madden JV, J., Evans, C.J., Tyler, A.N., Esch, P.S., Boehlen, P.; Makk, G.; Weber, E.  
 J. Neurochem. 56, 191-1920, 1991  
 A;Title: Isolation and characterization of opioid peptides from rabbit cerebellum.  
 A;Reference number: A60224; MUID:91225680; PMID:2027006  
 A;Accession: A60224  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-7 <MAU>  
 C;Superfamily: Proenkephalin  
 C;Keywords: neuropeptide; opioid peptide

Query Match 28.4%; Score 19; DB 2; Length 7;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	2	YGSF 5	
Db	1	YGFP 4	

RESULT 14

A41117  
 acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)  
 C;Species: Naja naja oxiana (Asian cobra, Oxus cobra)  
 C;Date: 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 09-Jul-2004  
 C;Accession: A41117  
 R;Kreinikamp, H.J.; Weise, C.; Raba, R.; Havikaar, A.; Bucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo marmorata  
 A;Reference number: A41117; MUID:91298772; PMID:2068091  
 A;Accession: A41117  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-8 <KRE>  
 A;Cross-references: UNIPROT:Q7LZ27  
 C;Keywords: carboxylic ester hydrolase

Query Match 28.4%; Score 19; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	7	SELW 10	
Db	2	AEMW 5	

RESULT 15

A60410  
 beta-neendorphin / dynorphin precursor - guinea pig  
 N;Alternative names: alpha-neoendorphin; proenkephalin B precursor  
 C;Species: Cavia porcellus (guinea pig)  
 C;Accession: A60410  
 C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 21-Jan-2000  
 R;Murphy, R.; Turner, C.A.  
 Peptides 11, 65-68, 1990  
 A;Title: Isolation and microsequence analysis of guinea pig alpha-neo-endorphin.  
 A;Reference number: A60410; MUID:90259864; PMID:2342991  
 A;Accession: A60410  
 A;Molecule type: protein  
 A;Residues: 1-10 <MUR>  
 A;Reference number: A60410; MUID:90259864; PMID:2342991  
 C;Keywords: neuropeptide; opioid peptide

Query Match 28.4%; Score 19; DB 2; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	2	YGSF 5	
Db	1	YGFP 4	

Search completed: August 3, 2005, 19:00:52  
 Job time : 40 secs

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OM protein - protein search, using SW model

Run on: August 3, 2005, 18:41:50 ; Search time 65 seconds  
 (without alignments)  
 37.242 Million cell updates/sec

Title: US-10-088-681-2

Perfect score: 67  
 Sequence: 1 BYGSPFSELWTS 12

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 4233

Minimum DB seq length: 0  
 Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

Database : UniProt\_03\_\*  
 1: uniprot\_sprot:  
 2: uniprot\_trembl:  
 \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	24	35.8	11 2 077995	077895 oreochromis
2	24	35.8	11 2 077996	077896 oreochromis
3	23	34.3	11 2 P83337	P83337 lactobacill
4	22	32.8	12 2 Q9TRT7	Q9TRT7 bos taurus
5	21	31.3	9 2 Q95553	Q95553 homo sapien
6	20	29.9	10 2 Q6L662	Q6L662 homo sapien
7	20	29.9	10 2 P9276	P9276 bipes bipor
8	20	29.9	11 1 CORZ PERAM	P11496 deripilanea
9	20	29.9	11 2 Q77994	Q77894 oreochromis
10	20	29.9	11 2 Q77998	Q77898 oreochromis
11	20	29.9	11 2 Q656G7	Q85cg7 binailoa tom
12	20	29.9	12 2 Q66664	Q66664 macropus rho
13	20	29.9	12 2 Q61331	Q61331 mus musculi
14	19	28.4	6 1 FARQ MONEX	P41966 moniezia ex
15	19	28.4	8 2 Q99M0	Q99mn0 mus musculi
16	19	28.4	8 2 Q7L227	Q1227 naja oxiana
17	19	28.4	10 2 Q9T447	Q9tr47 bos taurus
18	19	28.4	10 2 Q8SIC6	Q8shc6 furcifer be
19	19	28.4	11 2 Q9UQ46	Q9UQ46 homa sapien
20	19	28.4	12 2 Q53779	Q53579 rhodobacter
21	19	28.4	12 2 Q65579	Q65579 rattus norv
22	18	26.9	8 2 Q681R1	Q881f1 myrmotherul
23	18	26.9	8 2 Q681G3	Q881g3 sakesphorus
24	18	26.9	9 1 LITR PHYRO	P08946 phyllomedus
25	18	26.9	9 2 Q9HJY3	Q9h3y3 homa sapien
26	18	26.9	9 2 Q8H221	Q8h221 cyanophaghe
27	18	26.9	9 2 Q90550	Q90350 gb virus c/
28	18	26.9	10 1 AKHJ LOCM1	P81626 locusta mig
29	18	26.9	10 2 Q7M465	P07m465 platyptilea
30	18	26.9	10 2 Q8SHB1	Q8shb1 rhampholeon
31	18	26.9	10 2 Q8SHB4	Q8shb4 furcifer ve

ALIGNMENTS

Q8shb7 furcifer ou  
 Q8shc0 furcifer la  
 Q8shc1 furcifer la  
 LPM THETH  
 P0524 thermus the  
 P41333 scyliorhinu  
 Q9el1 homo sapien  
 Q9el2 larva glauc  
 Q9el3 solanum tub  
 Q80x04 rattus sp.  
 Q8shc3 furcifer la  
 Q8shc4 woodchick h  
 Q8uw0 rana catesbe  
 Q9dx0 grub canade  
 Q9el2 larva glauc  
 Q9el3 purfinus gr  
 Q9el4 phalacrocor  
 Q1203 capine art  
 P1987 leucophaea  
 Q8ge6 procambarus  
 P16353 heliothis z  
 P1270 jatropa mu  
 Q9u33 canis famili  
 Q715u5 ovis aries  
 P67790 zophobas ru  
 Q40530 nicotiana  
 Q8ge6 procambarus  
 P16353 heliothis z  
 P1270 jatropa mu  
 Q9u33 canis famili  
 Q715u5 ovis aries  
 P67790 zophobas ru  
 Q40530 nicotiana  
 Q9el3 gallus gall  
 Q9el4 gallus gall  
 Q7fx5 plasmodes bim  
 P67786 prothopomri  
 Q70y67 prostranther  
 Q70y72 tetradeenia  
 P8186 padachirus  
 P82096 litoria rub  
 P67785 gryllus bim  
 P61855 prothopomri  
 Q70y67 romalea mic  
 P67786 pandanus bo  
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 Q70y67 varanus sal  
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 Q70y67 fuerska af  
 Q7m010 clostroidium  
 Q7x145 staphylococ  
 Q79nx9 hydrochoeru  
 Q79nx9 hydrochoeru  
 Q67721 rattus norv  
 P67787 heliothis 2  
 Q9mw43 homo sapien  
 Q9avc6 varanus pil  
 Q891d6 anolis sagr  
 Q7688 gecko gecko  
 Q83366 bacteriophag  
 Q83366 bacteriophag  
 Q9r5ml staphylococ  
 Q873ws tyramus me  
 Q773w6 terpsiphone  
 Q677w7 telophorus  
 Q677w8 tchagra sen  
 Q873w9 tchagra aus  
 Q873w9 tchagra aus  
 Q9r5ml staphylococ  
 Q873ws tyramus me  
 Q773w6 terpsiphone  
 Q677w7 telophorus  
 Q677w8 tchagra sen  
 Q873w9 tchagra aus  
 Q873w9 tchagra aus  
 Q873x0 rhodophone  
 Q873x1 rhodophone  
 Q873x2 pseudobias  
 Q673x3 priornops sc  
 Q673x4 priornops re  
 Q673x5 platyrhynch  
 Q673x6 oriolus xan

RESULT 1					
077895	PRELIMINARY;	PRT;	11 AA.		
ID					
077895					
AC	077895;				
DT	01-NOV-1998 (TREMBLrel. 08, Created)				
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DR	MHC class II B locus 12 (Fragment).				
OS	Oreochromis niloticus (Nile tilapia) (tilapia nilotica)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Osteichthyes; Cetacei; Acanthomorpha; Acanthopterygii; Perciformes; Labroidei; Osteoglossiformes; Cichlidae; Oreochromis.				
OC	NCBI_TaxID=8128;				
RN	[1]				
RP	SEQUENCE FROM N.A. PubMed=9649539;				
RX	Medline=9831513;				
RA	Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V., Figuerola F., Sultmann H., Klein J.;				
RT	"Linkage relationships and haplotype polymorphism among cichlid MHC class II B loci."				
RL	Genetics 149:1527-1537(1998).				
DR	EMBL; AF050005; AAC41344.1; -.				
FT	NON_TER 1 1				
FT	NON_TER 11 11				
SQ	SEQUENCE 11 AA; 1367 MW; 3F47C9EAT72045A3 CRC64;				
Query Match	35.8%; Score 24; DB 2; Length 11;				
Best Local Similarity	50.0%; Pred. No. 2.7e+03;				
Matches	4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;				
Qy	5 FSSELWTS 12				
Db	3 FWSSILWVA 10				
RESULT 2					
077896	PRELIMINARY;	PRT;	11 AA.		
ID					
AC	077896;				
DT	01-NOV-1998 (TREMBLrel. 08, Created)				
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)				
DT	01-NOV-2001 (TREMBLrel. 19, Last annotation update)				
DR	MHC class II B locus 12 (Fragment).				
OS	Oreochromis niloticus (Nile tilapia) (tilapia nilotica)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi; Actinopterygii; Neopterygii; Teleostei; Butelosteil; Neoteleostei; Osteichthyes; Cetacei; Acanthomorpha; Acanthopterygii; Perciformes; Labroidei; Osteoglossiformes; Cichlidae; Oreochromis.				
OC	NCBI_TaxID=8128;				
[1]					
RP	SEQUENCE FROM N.A. PubMed=9649539;				
RX	Medline=9831513;				
RA	Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V., Figuerola F., Sultmann H., Klein J.;				
RT	"Linkage relationships and haplotype polymorphism among cichlid MHC class II B loci."				
RL	Genetics 149:1527-1537(1998).				
DR	EMBL; AF050006; AAC41345.1; -.				
FT	NON_TER 1 1				
FT	NON_TER 11 11				
SQ	SEQUENCE 11 AA; 1359 MW; 3F47DB7A72685A3 CRC64;				
Query Match	35.8%; Score 24; DB 2; Length 11;				
Best Local Similarity	66.7%; Pred. No. 2.7e+03;				
Matches	4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;				
Qy	5 FSSELW 10				
Db	3 FWSSMLW 8				
RESULT 3					
P83537	PRELIMINARY;	PRT;	11 AA.		
ID					
AC	P83537;				
DT	01-JUN-2003 (TREMBLrel. 24, Created)				
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)				
DR	Unknown protein from 2D-page (Fragment).				
DE	Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).				
OS	Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.				
OC	NCBITaxonID=1625;				
RN	[1]				
RP	SEQUENCE, AND INDUCTION.				
RX	STRAIN-DSM 20451;				
RX	PubMed=12112860;				
RA	Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;				
RT	"High pressure effects step-wise altered protein expression in lactobacillus sanfranciscensis.";				
RL	Proteomics 2: 765-774(2002).				
CC	-I- INDUCTION: By elevated hydrostatic pressure.				
CC	-I- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown protein is: 65 kDa.				
CC	FT NON_TER 1 1				
FT	NON_TER 11 11				
SQ	SEQUENCE 11 AA; 1249 MW; D96C8231B771ADD9 CRC64;				
Query Match	34.3%; Score 23; DB 2; Length 11;				
Best Local Similarity	80.0%; Pred. No. 4.1e+03;				
Matches	4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
Qy	3 GSFFS 7				
Db	1 GSFFPA 5				
RESULT 4					
Q9TRT7	PRELIMINARY;	PRT;	12 AA.		
ID					
AC	Q9TRT7;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DR	15 kDa amyloid protein A homolog (Fragment).				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetariodactyla; Ruminantia; Pecora; Bovidae; Bovine; Bos.				
OC	NCBI_TaxID=9913;				
RN	[1]				
RP	SEQUENCE.				
RX	Medline=92132498; PubMed=1734497;				
RA	Veiby O.P., Slesteen K., Husby G., Nordstoga K.;				
RT	"Amino acid sequence analyses of non-AA proteins from amyloid fibrils of bovine kidney";				
RT	Scand. J. Immunol. 35: 63-69 (1992).				
FT	NON_TER 1 1				
FT	NON_TER 12 12				
SQ	SEQUENCE 12 AA; 1503 MW; 64CDB543C6DB4AE CRC64;				
Query Match	32.8%; Score 22; DB 2; Length 12;				
Best Local Similarity	57.1%; Pred. No. 6.6e+03;				
Matches	4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;				
Qy	4 SFSELW 10				
Db	1 SFSEXY 7				
RESULT 5					
095953	PRELIMINARY;	PRT;	9 AA.		
ID					

AC	095953;	Db	1 SVVSEKW 7	
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)	RESULT	7	
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)	P22576	PRELIMINARY;	
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	ID	P22576	
DE	Galactocerabrosidase (EC 3.2.1.46) (Fragment).	AC	P22576;	
OS	Homo sapiens (Human).	AC	P22576;	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)	
OX		DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
RN	[1]	DB	Cytochrome c oxidase subunit I (Fragment).	
RP	SEQUENCE FROM N.A.	GN	Name=CO1;	
RC	TISSUE=Brain;	OS	Bipes biporus (Baja worm lizard).	
RA	Lilli L. Torchiana B., Finocchiaro G.;	OG	Mitochondrion;	
RL	Submitted (Nov-1996) to the EMBL/GenBank/DBJ databases.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
DR	EMBL: U77631; AAD15624; 1; -.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bipedidae; Bipes.	
DR	GO: GO-0004336; P:galactosylceramide activity; IEA.	OX	NCBITaxID=52188;	
DR	GO; GO-0016798; P:hydrolase activity, acting on glycosyl bonds; IEA.	RN	[1]	
KW	Glycosidase; Hydrolase.	RP	SEQUENCE FROM N.A. PubMed=9000757;	
FT	NON_TER 9 AA; 1069 MW; 374FB2ADC2C693C8 CRC64;	RX	Medline=97153826; Pubmed=9000751;	
SO	SEQUENCE 9 AA; 1069 MW; 374FB2ADC2C693C8 CRC64;	RA	Macey J.R., Larson A., Ananjeva N.B., Pang Z., Papenfuss T.J.;	
Query Match	31.3%; Score 21; DB 2; Length 9;	RT	"Two novel gene orders and the role of light-strand replication in rearrangement of the vertebrate mitochondrial genome.";	
Best Local Similarity	37.5%; Pred. No. 1.6e+06;	RL	Mol. Biol. Evol. 14:91-104(1997).	
Matches	3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	RN	[2]	
QY	3 GSFPSELM 10	RP	SEQUENCE FROM N.A. Medline=97153820; Pubmed=9000751;	
Db	2 GRPVADIN 9	RX	Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;	
RESULT	6	RA	"Replication slippage may cause parallel evolution in the secondary structures of mitochondrial transfer RNAs";	
06LA62	PRELIMINARY; PRT; 10 AA.	RT	Mol. Biol. Evol. 14:30-39(1997).	
ID	06LA62;	RL	DR	EMBL: U71135; AAC48271; 1; -.
AC	06LA62; 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	DR	PIR; TI3888; TI3838;	
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	DR	GO; GO-0005739; C:mitochondrion; IEA.	
DE	Aminoride-sensitive epithelial sodium channel gamma subunit (Fragment).	RN	Mitochondrion.	
DB	(Fragment)	FT	NON_TER 10 AA; 1176 MW; 5B3580C9D5A411A7 CRC64;	
GN	Name=SCNN1G;	SO	SEQUENCE 10 AA; 1176 MW; 5B3580C9D5A411A7 CRC64;	
OS	Homo sapiens (Human).	QY	29.9%; Score 20; DB 2; Length 10;	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DB	Best Local Similarity 100.0%; Pred. No. 1.2e+04; Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DN	6 SFPS 9	
OX		RN		
RN	[1]	RP	SEQUENCE FROM N.A. MEDLINE=96321599; PubMed=8824247; DOI=10.1074/jbc.271.42.26062;	
RP	SEQUENCE FROM N.A. MEDLINE=96321599; PubMed=8824247; DOI=10.1074/jbc.271.42.26062;	RESULT	8	
RX	Thomas C.P., Dogett N.A., Fisher R., Stokes J.B.;	CORZ_PERAM	CORZ PERAM	
RT	"Genomic organization and the 5' flanking region of the gamma subunit of the human amiloride-sensitive epithelial sodium channel.";	ID	ID-CORZ PERAM	
RT	J. Biol. Chem. 271:26062-26066(1996).	AC	P11496;	
RL		DT	01-OCT-1989 (Rel. 12, Created)	
RN	[2]	DT	01-FEB-1994 (Rel. 28, Last sequence update)	
RP	SEQUENCE FROM N.A. MEDLINE=98316780; PubMed=2654208; Ludwig M., Bolkenius U., Wickert L., Marven P., Bidlingmaier F.;	DT	05-JUL-2004 (Rel. 44, Last annotation update)	
RX	"Structural organization of the gene encoding the alpha-subunit of the human amiloride-sensitive epithelial sodium channel.";	DB	DB	
RT	Hum. Genet. 102:576-581(1998).	DN	05-JUL-2004 (Rel. 44, Last annotation update)	
RL	DR	RN	Corazonin.	
RP	EMBL; 292982; CAB07506; 1; -.	OS	Periplaneta americana (American cockroach); Insecta; Pterygota; OC	
DR	GO; GO-0005216; F:ion channel activity; IEA.	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; OC	
KW	Ionic channel.	OC	Blattidae; Periplaneta.	
FT	NON_TER 1 1	OX	NCBI_TaxID=6978;	
FT	NON_TER 10 10	RN	[1]	
SO	SEQUENCE 10 AA; 1157 MW; DBAFFF83733B05A2 CRC64;	RP	SEQUENCE.	
Query Match	29.9%; Score 20; DB 2; Length 10;	RC	TISSUE-corpora cardiaca;	
Best Local Similarity	57.1%; Pred. No. 1.2e+04;	RX	MEDLINE=8935572; PubMed=2753132; DOI=10.1016/0014-5793(89)80727-6;	
Matches	4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	RA	Veenstra J.A.;	
QY	4 SFPS 10	RT	"Isolation and structure of corazonin, a cardioactive peptide from the American cockroach.";	
QY	4 SFPS 10	RL	FEBS Lett. 250:231-234(1989).	
QY	4 SFPS 10	CC	-1- FRCTION: Cardioactive peptide. Corazonin is probably involved in the physiological regulation of the heart beat.	
QY	4 SFPS 10	CC	-1- SUBCELLULAR LOCATION: Secreted.	
QY	4 SFPS 10	DR	PR; S05002; S05002.	
QY	4 SFPS 10	KW	Amidation; Direct protein sequencing; Neuropeptide;	

KW	Pyrrolidone carboxylic acid.	FT	NON_TER	1	1	
FT		FT	NON_TER	11	11	
MOD_RES	1	FT	SEQUENCE	11 AA;	1367 MW;	3F47DC0A62C045A3 CRC64;
SQ	11	11	SEQUENCE	11 AA;	1367 MW;	CRC64;
Query Match	Best Local Similarity 29.9%; Score 20; DB 1; Length 11; Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	Score 20; DB 2; Length 11; Pred. No. 1.3e+04; Mismatches 1; Indels 0; Gaps 0;				
Qy	6 FSPRLWTS 12	Db	5 YRGWWTN 11			
RESULT 9						
077894	PRELIMINARY;	PRT;	11 AA.			
ID	077894	AC	077894;	DT	01-NOV-1998 (TREMBrel. 08, Created)	
AC		DT		01-NOV-1998 (TREMBrel. 08, Last sequence update)		
AC		DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)			
DE	MHC class II B locus 12 (Fragment).	DE	MHC class II B locus 12 (Fragment).	DE	Transcriptional activator (Fragment).	
OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).	OS	Name=ac2;	GN		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Cichlidae; Oreochromis.	OC	Sinaloa tomato leaf curl virus.	OS		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Cichlidae; Oreochromis.	OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.	OC		
OX	[1]	OX	NCBI_TaxID=8128;	OX		
RP	SEQUENCE FROM N.A.	RP		RP		
RX	Medline=98315113; PubMed=6649539;	RX		RX		
RA	Malaga-Tillo E., Zaleska-Rutkowska Z., McAndrew B., Vincek V.,	RA		RA		
RA	Figuerola F., Sultmann H., Klein J.;	RA		RA		
RT	"Linkage relationships and haplotype polymorphism among cichlid MHC genes II B loci".	RT		RT		
RT	Genetics 149:1527-1537(1998).	RT		RT		
RL		RL		RL		
DR	EMBL: AF050004; AAC41343.1; -.	DR		DR		
FT	NON_TER 1	FT		FT		
FT	NON_TER 1	FT		FT		
SQ	SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;	SQ		SQ		
Query Match	Best Local Similarity 29.9%; Score 20; DB 2; Length 11; Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	Query Match	Best Local Similarity 29.9%; Score 20; DB 2; Length 11; Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	Query Match	Best Local Similarity 29.9%; Score 20; DB 2; Length 11; Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	
Qy	5 FSEELW 10	Db	4 SFSELW 11	Qy	4 SFSELW 11	
RESULT 10						
077898	PRELIMINARY;	PRT;	11 AA.			
ID	077898	AC	077898;	DT	01-NOV-1998 (TREMBrel. 08, Created)	
AC		DT		01-NOV-1998 (TREMBrel. 08, Last sequence update)		
AC		DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)			
DE	MHC class II B locus 12 (Fragment).	DE	Glucose-6-phosphate dehydrogenase (Fragment).	DB		
OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).	OS	Name=G6PD;	GN		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Cichlidae; Oreochromis.	OC	Macropus robustus robustus.	OS		
OC	Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Cichlidae; Oreochromis.	OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.	OC		
OX	[1]	OX	Macropus robustus robustus.	OX		
RN	NCBI_TaxID=8128;	RN		RN		
RP	SEQUENCE FROM N.A.	RP		RP		
RX	Medline=98315113; PubMed=6649539;	RX		RX		
RA	Malaga-Tillo E., Zaleska-Rutkowska Z., McAndrew B., Vincek V.,	RA		RA		
RA	Figuerola F., Sultmann H., Klein J.;	RA		RA		
RT	"Linkage relationships and haplotype polymorphism among cichlid MHC genes II B loci".	RT		RT		
RT	Genetics 149:1527-1537(1998).	RT		RT		
DR	EMBL: AF050008; AAC41347.1; -.	DR		DR		
RESULT 11						
065CG7	PRELIMINARY;	PRT;	11 AA.			
ID	065CG7	AC	065CG7;	DT	25-OCT-2004 (TREMBrel. 28, Created)	
AC		DT		25-OCT-2004 (TREMBrel. 28, Last sequence update)		
AC		DT	25-OCT-2004 (TREMBrel. 28, Last annotation update)			
DE	Transcriptional activator (Fragment).	DE		DE		
GN	Name=ac2;	GN		GN		
OS	Sinaloa tomato leaf curl virus.	OS		OS		
OC	Nicaragua; ssDNA viruses; Geminiviridae; Begomovirus.	OC		OC		
OX	[1]	OX	NCBI_TaxID=71186;	OX		
RN	SEQUENCE FROM N.A.	RN		RN		
RC	STRAIN=N13;	RC		RC		
RA	Rojas A., Kvarnveden A., Rodriguez D., Valkonen J.P.T.;	RA		RA		
RA	"A mixture of begomoviruses in Severe leaf curl-affected tomatoes in Nicaragua." Submitted (SEP-2002) to the EMBL/GenBank/DDJB databases.	RA		RA		
RL		RL		RL		
DR	EMBL: AJ508781; CAD48523.1; -.	DR		DR		
FT	NON_TER 1	FT		FT		
SQ	SEQUENCE 11 AA; 1356 MW; 861BC90602D379DS CRC64;	SQ		SQ		
Query Match	Best Local Similarity 29.9%; Score 20; DB 2; Length 11; Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	Query Match	Best Local Similarity 29.9%; Score 20; DB 2; Length 11; Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	Query Match	Best Local Similarity 29.9%; Score 20; DB 2; Length 11; Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	
Qy	4 SFSELW 11	Db	4 SFSELW 11	Qy	4 SFSELW 11	
RESULT 12						
046664	PRELIMINARY;	PRT;	12 AA.			
ID	046664	AC	046664;	DT	01-JUN-1998 (TREMBrel. 05, Created)	
AC		DT		01-JUN-1998 (TREMBrel. 06, Last sequence update)		
AC		DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)			
DB	Glucose-6-phosphate dehydrogenase (Fragment).	DB		DB		
GN	Name=G6PD;	GN		GN		
OS	Macropus robustus robustus.	OS		OS		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.	OC		OC		
OX	[1]	OX		OX		
RN	NCBI_TaxID=35580;	RN		RN		
RP	SEQUENCE FROM N.A.	RP		RP		
RX	Medline=97224585; PubMed=9060417;	RX		RX		
RA	Loebel D.A., Johnston P.G.;	RA		RA		
RA	"Analysis of the intron-exon structure of the G6PD gene of the wallaroo (Macropus robustus) by polymerase chain reaction."	RA		RA		
RT		RT		RT		
RT	Mamm. Genome 8:146-147(1997).	RT		RT		
DR	EMBL: US3774; AAC48799.1; -.	DR		DR		
FT	NON_TER 1	FT		FT		
SQ	SEQUENCE 12 AA; 1430 MW; D42A9C84E3CB1AA9 CRC64;	SQ		SQ		
Query Match	Best Local Similarity 29.9%; Score 20; DB 2; Length 12; Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	Query Match	Best Local Similarity 50.0%; Score 20; DB 2; Length 12; Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	Query Match	Best Local Similarity 50.0%; Score 20; DB 2; Length 12; Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
Qy	5 FFSELW 10	Db	3 FWSIVW 8	Qy	5 FFSELW 10	

Qy 3 GSFPSE 8  
| : |  
ID Q61331 PRELIMINARY; PRT; 12 AA.  
AC 2 GGYFDE 7

RESULT 13

Q61331 PRELIMINARY; PRT; 12 AA.

ID Q61331; DT 01-NOV-1996 (TREMBrel. 01, Created)  
DT 01-MAY-1999 (TREMBrel. 10, Last sequence update)  
DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)

DE N-acetylglucosamine beta1-4 galactosyl transferase (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=1090;  
RN [1] SEQUENCE FROM N.A.  
RP MEDLINE=89033997; RX  
RA Nakazawa K.; Ando T.; Kimura T.; Narimatsu H.;  
RT Cloning and sequencing of a full-length cDNA of mouse N-  
acetylglucosamine (beta 1-4)galactosyltransferase.;  
RL J. Biochem. 104:165-168(1988).  
DR ENBL; D001217.1;-;  
DR GO:0003445; F:N-acetylglucosamine synthase activity; IEA.  
DR GO:0016577; F:transferase activity, transferring glycosyl . . ; IEA.  
KW Glycosyltransferase; Transferase.  
FT NON\_TER 1 12  
FT NON\_TER 1 12  
SQ SEQUENCE 12 AA; 1203 MW; 304EA4066838728 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 WTS 12  
Db 1 WTS 3

RESULT 14

FARP\_MONEX STANDARD; PRT; 6 AA.

ID FARP\_MONEX  
AC P41966;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DB FMRFamide-like neuropeptide FMRF-amide.  
OS Moniezia expansa (Sheep tapeworm).  
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;  
OC Cyclophyllidae; Anoplocephalidae; Moniezia.  
OC NCBI\_TaxID=28841;  
RN [1] SEQUENCE.  
RP MEDLINE=93312289; PubMed=8323531;  
RA Maule A.G.; Shaw C.; Halton D.W.; Thim L.;  
RT "GNRFamide: a novel FMRFamide-immunoreactive peptide isolated from  
the sheep tapeworm, *Moniezia expansa*";  
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
family.  
DR PIR: A43129; A43129;  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 6 6  
SEQUENCE 6 AA; 787 MW; 69D49C9C481000 CRC64;

Query Match 28.4%; Score 19; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: August 3, 2005, 18:57:22  
Job time : 166 sec8

Qy 3 GSFP 6  
| : |  
ID Q99MNO PRELIMINARY; PRT; 8 AA.  
AC 099MNO;  
DT 01-JUN-2001 (TREMBrel. 17, Created)  
DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)

DE Adenosine deaminase tRNA-specific 1 (Fragment).  
GN Name=ADAT1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=1090;  
RN [1] SEQUENCE FROM N.A.  
RP MEDLINE=21231131; RX  
RA Maas S.; Kim Y.G.; Rich A.;  
RT "Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two  
tRNA synthetases";  
RL Mamm. Genome 12:387-393(2001).  
DR EMBL; AP32804; RAK19310.1; -.  
DR MGDB; MGDB:1533631; ADAT1.  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 936 MW; F4D05B1AADCC1B376 CRC64;

Query Match 28.4%; Score 19; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LWTS 12  
Db 1 MWTA 4

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OM protein - protein search, using Bw model									
Copyright (c) 1993 - 2005 Compugen Ltd.									
GenCore version 5.1.6									
Run on:	August 3, 2005, 18:42:40	, search time 159 seconds	(without alignments)	29.189 Million cell updates/sec	27	28	28	41.8	10
Title:	US-10-088-681-2	27	28	28	41.8	10	8	ADK05533	41.8
Perfect score:	67	27	40.3	6	2	AAR9913	9	9	9
Sequence:	1 EYGSFSELSWTS 12	27	40.3	6	3	AAY93379	11	3	10
Scoring table:	BLOSUM62	27	40.3	6	6	ABR4627	11	7	11
Gapext:	Gapext 0.5	27	40.3	6	6	ABP3169	9	2	9
Searched:	2105692 seqs, 386760381 residues	27	40.3	6	6	ABR46507	9	2	9
Total number of hits satisfying chosen parameters:	520583	27	40.3	6	6	ABR46507	32	27.5	32
Minimum DB seq length:	0	27	40.3	6	6	ABR46507	31	27.5	31
Maximum DB seq length:	12	27	40.3	6	6	ABR46507	30	27.5	30
Post-processing:	Minimum Match 0%	27	40.3	6	6	ABR46507	29	27.5	29
Maximum Match 100%									
Listing first 100 summaries									
Database :	A_Geneseq_16Dec04:*	27	40.3	6	6	ADJ73323	6	7	6
1:	geneseqD1980s:*	27	40.3	6	6	ADJ2957	6	8	6
2:	geneseqD2000s:*	27	40.3	6	6	ADJ5191	6	8	6
3:	geneseqD2001s:*	27	40.3	6	6	AAR8921	7	2	7
4:	geneseqD2002s:*	27	40.3	6	6	AAR9925	5	5	5
5:	geneseqD2003as:*	27	40.3	6	6	AAR9925	5	5	5
6:	geneseqD2003bs:*	27	40.3	6	6	AAR9925	5	5	5
7:	geneseqD2004bs:*	27	40.3	6	6	AAR9925	5	5	5
8:	geneseqD2004gs:*	27	40.3	6	6	AAR9925	5	5	5
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	27	40.3	6	6	AAR9925	5	5	5	5
SUMMARIES									
Result No.	Score	Query Match length	DB ID	Description	27	40.3	6	6	5
1	55	82.1	12 4	AAB86005	70	40.3	10	8	ADP80344
2	34	50.7	6 4	AAB97294	71	40.3	10	8	ADP80344
3	34	50.7	6 5	AAB97294	72	40.3	12	2	AAR611
4	34	50.7	6 8	ADP42242	73	40.3	12	2	AAW36888
5	34	50.7	8 3	AAB09130	74	40.3	12	2	AAW36888
6	31	46.3	10 8	ADK05671	75	40.3	12	2	AAW37188
7	31	46.3	10 8	ADK05188	76	40.3	12	2	AAW37188
8	30	44.8	6 6	ABR45515	77	40.3	12	2	AAW37188
9	30	44.8	9 2	AAW71938	78	40.3	12	3	AAB37076
10	30	44.8	10 2	AAW37198	79	40.3	12	3	AAB37087
11	30	44.8	10 2	AAW37198	80	40.3	12	3	AAB37087
12	30	44.8	10 6	AB61398	81	40.3	12	3	AAB37075
13	30	44.8	10 6	ABO19036	82	40.3	12	5	ABY31170
14	30	44.8	10 7	ADG71874	83	40.3	12	5	ABY31170
15	30	44.8	10 7	ADG71874	84	40.3	12	5	ABY31170
16	29	43.3	7 2	AAY33139	85	40.3	12	5	ABY31170
17	29	43.3	10 5	AAU93215	86	40.3	12	5	ABY31170
18	29	43.3	11 6	ABJ37125	87	40.3	12	5	ADT73324
19	29	43.3	12 4	ABM0568	88	40.3	12	7	ADT73336
20	28	41.8	6 6	ABR4459	89	40.3	12	7	ADT73337
21	28	41.8	7 2	ADP68305	90	40.3	12	7	ADT73337
22	28	41.8	8 8	ADK09492	91	40.3	12	8	ADT31725
23	28	41.8	9 2	AAV04678	92	40.3	12	8	ADT31725
24	28	41.8	9 2	ADK05532	93	40.3	12	8	ADT31725
25	28	41.8	9 8	ADK05531	94	40.3	12	8	ADT31725

Abd059533	Human pap
Adk09606	Human pap
Aav93379	Binding m
Adf35467	MCP 603
Aar8533	Light cha
Aar95306	Light cha
Aar89913	p53 /Rbm2
Aaw13606	p53 prote
Abp17074	Mdm /adm a
Abp27159	Mdm /adm a
Abp46627	Staphyloc
Adj15118	CH1 dele
Aar9921	Antibody
Aar89925	p53 bindi
Aar73432	Human p53
Adt73323	Mdm /adm a
Adz15297	CH1 dele
Adj15118	CH1 dele
Aee31316	Human p53
Aee1395	Human p53
Adk09595	Human pap
Adz28798	Human cel
Aau37119	Human onc
Aee31317	Human p53
Aar89917	Human p53
Aaw13605	p53 prote
Aad78885	Human p53
Adz48959	Peptide #
Adh64792	H1A bindi
Aau26842	Human Leu
Adg47923	Pancreati
Adg60923	Minatur
Adg64806	H1A bindi
Adp80368	Human HLA
Aat8611	Anti-ELAM
Aav26888	ELAM-1 bi
Aau7152	Human Leu
Aab26842	Human Leu
Aam52269	Minatur
Aaw37189	Human onc
Aab1706	Mdm /hdm a
Aab17087	Mdm /hdm a
Aab17088	Mdm /hdm a
Aab17075	Mdm /hdm a
Aab57310	Mdm /hdm a
Aab57318	Mdm /hdm a
Aab73171	Mdm /hdm a
Aab73182	Mdm /hdm a
Aab17334	Mdm /hdm a
Aab17336	Mdm /hdm a
Aab17337	Mdm /hdm a
Aab57325	Mdm /hdm a
Aad34264	Wild type
Adj152959	CH1 dele
Akj52971	CH1 dele
Akj52970	CH1 dele
Akj52958	CH1 dele
Akj51920	CH1 dele
Aej51932	CH1 dele
Aej51931	CH1 dele
Aej51919	CH1 dele
Aej51919	CH1 dele
Aer25372	Peptide #

99 26 38.8 5 2 AAR9912  
100 26 38.8 5 2 AAW52022

**ALIGNMENTS**

**RESULT 1**  
ID AAB86005 standard; peptide; 12 AA.  
XX  
AC AAB86005;  
XX  
DT 12-JUL-2001 (first entry)  
XX  
DE DCM-associated peptide #5.  
XX  
KW DCM; dilatative cardiomyopathy; autoantibody; cardiant; betal-1 adrenergic activated antibody; immunosuppressive.  
KW  
OS Synthetic.  
XX  
PN WO200121660-A1.  
XX  
PD 29-MAR-2001.  
XX  
PF 21-SEP-2000; 2000WO-EP009241.  
XX  
PR 21-SEP-1999; 99EP-00118630.  
PR 21-SEP-1999; 99EP-00118631.  
XX  
PA (BIOM-) INST APPLIED BIOMEDICINE.  
XX  
PI Chaplin JW;  
XX  
DR WPI; 2001-316435/33.  
XX  
PT B cell clonal toxin useful for treating autoimmune disorders such as Grave's disease, myocardial infarction, Crohn's disease, multiple sclerosis, comprises a group that causes toxin to be internalized by B cell.  
PT  
XX  
PS Disclosure; Page 26; 46pp; English.

XX  
CC This invention relates to a B cell clonal toxin. The toxin is made from two moieties, the first causes the toxin to be internalised by a B cell, and the second is a biologically acceptable toxin. The invention includes a method for inactivating/killing an antigen specific B cell. A target B cell is contacted with an effective amount of a B cell clonal toxin. The method is useful for selective immunosuppression in conditions characterised by the presence of an unwanted or deleterious immune response, e.g. in the treatment of antigen specific antibody mediated disease conditions. Use of the B cell clonal toxin can result in immunosuppressive; antiinflammatory; antiallergic; viricide; antidiabetic ; thyromimetic; antithyroid; vasotropic; cardiant; antiulcer; neuroprotective; antirheumatic; antiarthritic; dermatological; ophthalmological; nephrotoxic; allergy; autoimmune disorder; skin diseases; autoimmune endocrinopathy; vasculitic syndrome; cardiovascular disease; immunohaematologic disorder; neurologic disease; gastrointestinal disease; collagen vascular disease; renal diseases; pulmonary disease; and infertility disorders. The present sequence represents a betal-adrenoceptor epitope. An antibody response to this antigen is implicated in dilated cardiomyopathy, a disorder which may be treated using the toxin of the invention

XX  
SQ Sequence 12 AA;

Query Match 82.1%; Score 55; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GSPFSEWTS 12  
XX  
Db 2 GSPFSEWTS 11

XX  
SQ Sequence 6 AA;

Query Match 50.7%; Score 34; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Mismatches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EVGSFF 6  
XX  
Db 1 EVGSFF 6

**RESULT 2**  
ID AAB97294  
XX  
AC AAB97294;  
XX  
DT 13-AUG-2001 (first entry)  
XX  
DE Beta-adrenoceptor secondary loop epitope peptide #3.  
XX  
KW B cell; toxin; antigen specific; antibody mediated disease; virucide;

XX  
RESULT 3  
ID AAM47222 standard; peptide; 6 AA.

XX  
AC AAM47222;  
XX  
DT 12-FEB-2002 (first entry)  
XX  
DE Dilated cardiomyopathy; absorbents related peptide #2.  
XX  
KW Dilated cardiomyopathy; absorbent; betal adrenoreceptor;  
M2 muscarine receptor; antibody.  
OS Synthetic.  
XX  
PN WO200176662-A1.  
XX  
PD 18-OCT-2001.  
XX  
PP 09-APR-2001; 2001WO-JP003926.  
XX  
PR 07-APR-2000; 2000JP-00106915.  
XX  
PA (KANF ) KANEKA CORP.  
XX  
PI Ogino E, Furuyoshi S, Hirai F, Nishimoto T;  
DR WPI; 2002-041274/05.  
XX  
PT Adsorbents for dilated cardiomyopathy, comprises an immobilized compound capable of selectively removing antibodies against approximately b1 adrenoreceptor and/or M2 muscarine receptors in body fluid without pretreatment.  
XX  
PS Claim 3; Page 21; 37pp; Japanese.  
XX  
CC The present invention relates to a method of immobilising an adsorbent with a compound capable of binding to an antibody against betal adrenoreceptor and/or an antibody against M2 muscarine receptor on a water-insoluble support. The adsorbents, apparatus and method are useful for treating dilated cardiomyopathy by removing antibodies against betal adrenoreceptor and/or M2 muscarine receptor. The present sequence is a peptide described in the exemplification of the invention.  
XX  
SQ Sequence 6 AA:  
Query Match 50.7%; Score 34; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CC  
Qy 1 EVGSFF 6  
Db 1 EVGSFF 6  
XX  
RESULT 4  
ID ADP49242 standard; peptide; 6 AA.  
XX  
AC ADP49242;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Disease-associated autoantibody detection method peptide #1.  
XX  
KW cardiot; gynaecological; immunosuppressive; hypotensive; antipsoriatic;  
vasotrop; disease-associated autoantibody; antibody;  
G protein-coupled receptor.  
XX  
OS Unidentified.  
XX  
PN WO2004051280-A2.  
XX  
PD 17-JUN-2004.  
XX  
PP 28-NOV-2003; 2003WO-DE003988.

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XX  
PR 29-NOV-2002; 2002DE-01056897.  
PR 27-JAN-2003; 2003DE-01003120.  
PR 13-JUN-2003; 2003DE-01027066.  
XX  
PA (DELB-) DEBRUCK CENT MOLEKULARE MEDIZIN MAX.  
XX  
PI Wallukat G;  
XX  
DR WPI; 2004-450802/42.  
XX  
PT Detecting disease-associated autoantibodies against G protein-coupled receptors, useful for diagnosing e.g. cardiomyopathy, comprises an enzymatic or color reaction.  
XX  
PS Claim 12; Page 49; 57pp; German.  
XX  
CC The present invention relates to a method for detecting disease-associated autoantibodies (Ab) directed against G protein-coupled receptors. This comprises treating a body fluid with a denaturing agent, treating the precipitate formed with a biotin-containing peptid having the (partial) sequence of a first and/or second loop of a G protein-coupled receptor, incubating the mixture with a carrier coated by (strept)avidin, washing the carrier and incubating it with labeled anti-immunoglobulin G (IgG) antibody subclasses, and performing an enzymatic or colour reaction. The method is used to detect Ab associated with dilative or Chagas cardiomyopathy, myocarditis, pre-eclampsia, humoral kidney rejection, malignant, essential, refractory or pulmonary hypertension, psoriasis and Raynaud's syndrome. The present invention is a peptide which can be used in the method of the invention.  
XX  
SQ Sequence 6 AA:  
Query Match 50.7%; Score 34; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CC  
Qy 1 EVGSFF 6  
Db 1 EVGSFF 6  
XX  
RESULT 5  
ID AAB09130  
ID AAB09130 standard; protein; 8 AA.  
XX  
AC AAB09130;  
XX  
DT 06-AUG-2003 (revised)  
DT 30-AUG-2000 (first entry)  
XX  
DE Hepatitis GB virus protein sequence SEQ ID NO:252.  
XX  
KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection; detection; characterisation; hepatitis.  
OS Hepatitis GB virus.  
XX  
PN US6051374-A.  
XX  
PD 18-APR-2000.  
XX  
PP 07-JUN-1995; 95US-00488445.  
XX  
PR 14-FEB-1994; 94US-00196030.  
PR 13-MAY-1994; 94US-0024654.  
PR 29-JUL-1994; 94US-0028314.  
PR 23-NOV-1994; 94US-00344185.  
PR 30-JAN-1995; 95US-00377557.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX

PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;  
 PT Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;  
 XX DR WPI; 2000-338307/29.

XX PT Detecting target hepatitis GB virus nucleic acid in a test sample suspected of containing HGBV comprises reacting the test sample the HGBV polynucleotide probe and detecting the complex that contains target HGBV.

PS Example 9; Col 331-332; 369pp; English.

XX CC The present invention describe a method for detecting target hepatitis GB virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of containing HGBV. The method involves reacting (T) with a HGBV polynucleotide probe (R) containing 15 contiguous nucleotides, and which selectively hybridises to the HGBV genome or its full complement, and detecting the complex that contains THN, indicating the presence of target HGBV. The method is used for detecting target HGBV nucleic acid in the test sample suspected of containing HGBV and for characterisation of newly ascertained etiological agent of non-A, non-B, non-C, non-D and non-E hepatitis causing agents collectively termed as hepatitis GB virus. AAAS270 to AAAS270 and AAAB0985 to AAB0940 represent nucleotide and protein sequences used in the exemplification of the present invention. (Updated on 06-AUG-2003 to correct OS field.)

XX SQ Sequence 8 AA;

Query Match	Score	DB	Length	Pred.	No.	Mismatches	Indels	Gaps
Best Local Similarity	50.7%	34	8	Pred.	1.8e+06	0	0	0
Matches	6					1	2	

QY 6 FSPWLTS 12  
 ID 1 FSHLWTS 7

XX RESULT 6  
 ADK0971  
 ID ADK09671 standard; peptide; 10 AA.

XX AC ADK09671;

XX DT 06-MAY-2004 (first entry)

XX DE Human papillomavirus peptide #1726.

XX KW pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; HPV.

XX OS Human papillomavirus.

XX PN WO2004011650-A2.

XX PD 05-FEB-2004.

XX PR 24-JUL-2003; 2003WO-EP008112.

XX PA (INTE-) INTERCELL AG.

XX PI Mattner F, Schmidt W, Habel A;

XX DR WPI; 2004-169243/16.

XX PS New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant; useful for treating or preventing an infection with the pathogenic virus.

XX Claim 18; Page 187; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the invention.

XX SQ Sequence 10 AA;

Query Match	Score	DB	Length	Pred.	No.	Mismatches	Indels	Gaps
Best Local Similarity	46.3%	31	10	Pred.	1.5e+02	2	0	0
Matches	5					1	2	

CC reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the invention.

XX PS Sequence 10 AA;

Query Match	Score	DB	Length	Pred.	No.	Mismatches	Indels	Gaps
Best Local Similarity	62.5%	31	10	Pred.	1.5e+02	2	0	0
Matches	5					1	2	

CC This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.

XX PS Claim 18; Page 192; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.

Oy	4	SPPSELWT	11	ID	AAW72493	standard; peptide; 9 AA.
:				XX	AAW72493;	
Db	1	SFFSRTWS	8	XX		
RESULT 8				DT	23-DEC-1998	(first entry)
ABR46515				DE	Dengue virus type-2 glycoprotein NS1 peptide for epitope mapping #38.	
ID				XX	Dengue virus type-2 glycoprotein NS1; dengue haemorrhagic fever; DHF;	
ABR46515 standard; peptide; 6 AA.				KW	dengue shock syndrome; DSS; Aedes aegypti; mosquito; antigen; vaccine;	
AC				KW	immunisation; immunoreactive; infection.	
ABR46515;				XX	Dengue virus.	
XX				XX	OS	
DT 10-JUN-2003 (first entry)				XX		
XX				XX		
DE Staphylococcus aureus CHIPS-related peptide #1705.				XX		
XX				XX		
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated Peptide Receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; KW gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; KW cardiotonic; neuroprotective; nootropic; dermatological; KW gynecological; immunosuppressive; anti-HIV.				XX		
XX				XX		
OS Staphylococcus aureus.				XX		
OS Synthetic.				XX		
PN WO2003006048-A1.				XX		
XX				XX		
PD 23-JAN-2003.				XX		
XX				XX		
PF 11-JUL-2001; 2001WO-EPO08004.				XX		
XX				XX		
PR 11-JUL-2001; 2001WO-EPO08004.				XX		
XX				XX		
PA (JARI-) JARI PHARM BV.				XX		
XX				XX		
PI Van Kessel CPM, Gosselaar-De Haas CUC, Kruytzer JAW;				XX		
XX				XX		
PI Van Strijp JAG;				XX		
XX				XX		
DR WPI; 2003-256333/25.				XX		
XX				XX		
PT Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in PT prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases.				XX		
XX				XX		
PS Disclosure; Page 17; 89pp; English.				XX		
XX				XX		
CC The present invention relates to peptides (ABR4811-ABR47162 and ABR47164 -ABR4785) derived from the Chemotaxis Inhibitory Protein (CHIPS) from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophil, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection				XX		
XX				XX		
SQ Sequence 6 AA:				XX		
Query Match Best Local Similarity Score 30; DB 2; Length 9; Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;				XX		
Oy     :	3	GSPFSELW	10	XX		
Db 1	GVFFFTNIW	8		XX		
RESULT 10				XX		
DT 02-NOV-1998 (first entry)				XX		
XX				XX		
DE LM609 grafted antibody V-H region CDR3 protein fragment #16.				XX		
XX				XX		
AC Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; primer; V-H region; CDR; complementarity determining region.				XX		
XX				XX		
OS Mus sp.				XX		
RESULT 9				XX		
AAW72493				XX		

XX  
PN WO9833919-A2.  
XX  
PD 06-AUG-1998.  
XX  
PR 30-JAN-1998; 98WO-US001826.  
XX  
PR 30-JAN-1997; 97US-00791391.  
XX  
PA (IXSY-) IXSYS INC.  
XX  
PT Rose WD, Glaser SM;  
XX  
DR WPI; 1998-437472/37.  
XX  
N-PSDB; ANV19877.  
XX  
Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
PT integrin - and related grafted antibodies based on murine monoclonal  
PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
PT angiogenesis or restenosis.  
XX  
Claim 62; Page 43; 12pp; English.  
XX  
AAW76007-W7040 are protein fragments of the grafted monoclonal antibody  
CC LM609 heavy and light chain variable region. LM609 and the antibody  
CC inhibit binding selectively to integrin alphavbeta3 and can be used to  
CC inhibit binding of alphavbeta3 to a ligand and thus block integrin-  
CC mediated signal transduction. This is useful in the treatment, prevention  
CC and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis  
CC and restenosis (but also e.g. (non-)immune inflammation, diabetic  
CC retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid  
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies  
CC contain non-murine framework regions so are suitable for use in humans.  
CC Enhanced types of LM609 have affinity more than 90 times greater than  
CC that of parent the parent antibody  
XX  
Sequence 10 AA:  
SQ  
Query Match Score 30; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 YGSPFSS 7  
Db 5 YGSFYS 10  
XX  
RESULT 11  
AAW37198  
ID AAW37198 standard; peptide; 10 AA.  
XX  
AC AAW37198;  
XX  
DT 20-JUL-1998 (first entry)  
XX  
DE Human oncogenic protein MDM2 binding Cys (Acrid) peptide derivative 2.  
XX  
KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
XX  
tumour; diagnosis; binding; viral infection.  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Modified-site 1  
FT /note= "N-terminal acetyl; Sulphydryl side-chain linked  
FT to 6-acryloyl-2-(dimethylamino)naphthalene"  
FT 10  
FT /note= "C-terminal amide"  
XX  
PN WO9801467-A2.  
XX  
PD 15-JAN-1998.

XX  
PF 04-JUL-1997; 97WO-EP003549.  
XX  
PR 05-JUL-1996; 96GB-00014197.  
PR 07-APR-1997; 97GB-00007041.  
XX  
PA (NOVUS ) NOVARTIS AG.  
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
XX  
Lane D, Boettger V, Boettger A, Picklesley S, Hochkeppel H;  
PI Garcia-Echeverria C, Chene P, Furet P;  
XX  
DR WPI; 1998-100996/09.  
XX  
PT Compounds binding to MDM2 protein and inhibit its interaction with p53 -  
PT useful in, e.g. diagnosis and treatment of cancer and viral infections  
PT and identifying binding agents.  
XX  
PS Example 2; Page 20; 45pp; English.  
XX  
CC This is a Cys (Acrid) peptide derivative capable of binding to a human  
oncogenic protein MDM2. The MDM2 binding peptide can specifically  
CC inhibit or block the binding of MDM2 to the human p53 protein, in vitro  
or in vivo. Inhibiting the interaction between the p53 and MDM2 can  
CC induce growth arrest or apoptosis in tumour cells comprising a wild-type  
p53 and non-elevated levels of MDM2. The peptides may be used to identify  
molecules that bind to MDM2 and to identify and design inhibitors of  
MDM2/p53 binding. They may also be used to purify binding partners  
especially MDM2, diagnose disease by measuring levels of MDM2 in blood of  
CC cancer and leukaemia patients and for treatment or prevention of disease  
CC involving p53/MDM2 interactions, especially tumours and viral infections.  
CC The peptides can be administered orally, rectally, or by injection. By interfering with MDM2/p53 interaction, the peptides can  
CC activate p53 function and accumulation in normal cells. The peptides  
CC which mimic the MDM2 binding site in p53, have a significantly greater  
CC blocking activity compared with wild-type p53  
XX  
Sequence 10 AA:  
SQ  
Query Match Score 30; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 GSFSELM 10  
Db 2 GPTESDLW 9  
XX  
RESULT 12  
ABB61398  
ID ABB61398 standard; peptide; 10 AA.  
XX  
AC ABB61398;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE Multiple mutant VH CDR3 #4.  
XX  
KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
inflammatory; cancer; retina; restenosis; osteoporosis.  
XX  
OS Unidentified.  
XX  
PN WO200078815-A1.  
XX  
PD 28-DEC-2000.  
XX  
PR 23-JUN-2000; 2000WO-US017454.  
XX  
PR 24-JUN-1999; 99US-00339922.  
XX  
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
XX



SQ Sequence 10 AA;

Query Match 44.8%; Score 30; DB 7; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGRRFS 7  
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 Db 5 YGSFYS 10

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RESULT 15

ADJ58055  
 ID ADJ58055 standard; peptide; 10 AA.  
 XX  
 AC  
 XX  
 ADJ58055;  
 DT 08-MAY-2004 (first entry)  
 XX  
 DE Murine LM609 heavy chain variable region (VH) CDR3 mutant peptide #15.  
 XX  
 KW Vitaxin; antibody; LM609; angiogenesis; restenosis; therapy;  
 KW variable region; mouse; mutant; mutein.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN US2004006213-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 16-JUN-2003; 2003US-00463847.  
 XX  
 PR 30-JAN-1997; 97US-00791391.  
 PR 30-JAN-1998; 98US-00016061.  
 XX  
 PA (IXSY-) IXSYS INC.  
 XX  
 PT Rueb WD, Glaser SM;  
 XX  
 DR WPI; 2004-081749/08.  
 XX  
 PT New Vitaxin antibody and a LM609 grafted antibody exhibiting selective binding affinity to alphavbeta3, useful for treating alphavbeta3-mediated diseases, e.g. angiogenesis or restenosis.  
 XX  
 PS Claim 62; SEQ ID NO 100; 69PP; English.  
 XX  
 CC The present invention provides a Vitaxin antibody and a LM609 grafted antibody exhibiting selective binding affinity to alpha-v-beta-3. The invention is useful for treating alpha-v-beta-3-mediated diseases such as angiogenesis and restenosis. The present sequence is murine LM609 antibody variable region CDR mutant peptide.  
 CC  
 XX  
 SQ Sequence 10 AA;

Query Match 44.8%; Score 30; DB 8; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGRRFS 7  
     |||||:  
 Db 5 YGSFYS 10

Search completed: August 3, 2005, 19:00:09  
 Job time : 162 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 18:54:46 ; Search time 42 Seconds  
(without alignments)  
21.328 Million cell updates/sec

Title: US-10-088-681-2  
perfect score: 67  
Sequence: 1 EYGSPPFSEWTS 12

Scoring table: BLOSUM62  
Gapext 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues  
Total number of hits satisfying chosen parameters: 135920

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Listing first 100 summaries

Database : Issued Patents AA:\*

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4: /cgn2_5.ptodata//1/iaa/5B_COMB.pep:*
5: /cgn2_6.ptodata/1/iaa/PCUTS_COMB.pep:*
6: /cgn2_6.ptodata/1/iaa/backFiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	34	50.7	8	4 US-08-469-2607-252
2	34	50.7	8	4 US-08-480-465-252
3	34	50.7	8	4 US-08-467-344-252
4	34	50.7	8	4 US-08-424-550-252
5	30	44.8	6	1 US-08-424-957-6
6	30	44.8	6	3 US-09-035-686-6
7	30	44.8	10	4 US-09-330-9228-100
8	30	44.8	10	4 US-09-016-061-100
9	30	44.8	11	1 US-08-424-957-42
10	30	44.8	11	3 US-09-030-686-42
11	29	43.3	7	4 US-09-595-6828-10
12	29	43.3	10	4 US-09-620-091-28
13	28	41.8	11	3 US-09-186-958-6
14	28	41.8	11	3 US-09-662-2718-6
15	28	41.8	11	4 US-09-081-276-6
16	27.5	41.0	9	1 US-08-300-386-50
17	27.5	41.0	9	3 US-09-645-50
18	27.5	41.0	9	5 PCT-US94-0250-50
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20	27	40.3	6	1 US-08-277-6602-2
21	27	40.3	6	1 US-08-424-957-2
22	27	40.3	6	3 US-09-030-686-50
23	27	40.3	6	4 US-09-081-975-1
24	27	40.3	6	4 US-09-420-0828-130
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91	26	38.8	11	1 US-08-277-6608-20
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3	37.3	6	1 US-07-943-709-38
2	37.3	6	1 US-07-943-709-39
1	37.3	6	1 US-07-943-709-40

## ALIGNMENTS

APPLICANT: GEORGE J. DAWSON

APPLICANT: GEORGE G. SCHLAUDER

APPLICANT: SURISH M. DESAI

APPLICANT: THOMAS P. LEARY

APPLICANT: ANTHONY SCOTT MUEHROFF

APPLICANT: JAMES C. ERKER

APPLICANT: SHERI L. BUIJK

APPLICANT: ISA K. MUSHAHWAR

TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 716

CORRESPONDENCE ADDRESS:

ADDRESSEE: ABBOTT LABORATORIES

STREET: 100 ABBOTT PARK ROAD

CITY: ABBOTT PARK

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,260A

FILING DATE: 2003-07-10

ATTORNEY/AGENT INFORMATION:

NAME: POREMBSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5527.PC.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 252:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

US-08-488-446-252

Query Match Score 34; DB 4; Length 8;  
Best Local Similarity 85.7%; Pred. No. 4.1e+05; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 0; Gaps 0;

QY 6 FSLWTS 12  
Db 1 FSHLWTS 7

RESULT 3

US-08-467-344A-252  
Sequence 252, Application US/08467344A

Patent No. 6586568

GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS

TAMI J. PILOT-MATIAS

GEORGE J. DAWSON

GEORGE G. SCHLAUDER

SURISH M. DESAI

THOMAS P. LEARY

ANTHONY SCOTT MUEHROFF

JAMES C. ERKER

SHERI L. BUIJK

ISA K. MUSHAHWAR

TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

REAGENTS AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 716

CORRESPONDENCE ADDRESS:

RESULT 2

US-08-488-446-252

Sequence 252, Application US/08488446

Patient No. 6554898

GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS

APPLICANT: TAMI J. PILOT-MATIAS

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,550B  
 FILING DATE: 20-JUL-1994  
 CLASSIFICATION: 435435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: POREMBSKI, PRISCILLA E.  
 REGISTRATION NUMBER: 33,207  
 REFERENCE/DOCKET NUMBER: 5527.PC.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 708-937-6365  
 TELEFAX: 708-938-6235

INFORMATION FOR SEQ ID NO: 252:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-424-550B-252

Query Match 50.7%; Score 34; DB 4; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 4.1e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 FSLIWTs 12  
 Db 1 FSHLWTS 7

RESULT 5  
 US-08-424-957-5  
 Sequence 6, Application US/08424957  
 Patent No. 5770377  
 GENERAL INFORMATION:  
 APPLICANT: Pickleley, Steven M.  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and p53  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,957  
 FILING DATE: 19-APR-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreyer, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WHD

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown

US-08-424-957-6

RESULT 4  
 US-08-424-550B-252  
 Sequence 252, Application US/08424550B  
 ;  
 ; PATENT NO. 6720166  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JOHN N. SIMONS  
 ; APPLICANT: TAMI J. PILOT-MATIAS  
 ; APPLICANT: GEORGE J. DAWSON  
 ; APPLICANT: GEORGE G. SCHLAUDER  
 ; APPLICANT: SURESH M. DESAI  
 ; APPLICANT: THOMAS P. LEARY  
 ; APPLICANT: ANTHONY SCOTT MUEHROFF  
 ; APPLICANT: JAMES C. ERKER  
 ; APPLICANT: SHERI L. BUTIJK  
 ; APPLICANT: ISA K. MUSHAHWAR  
 ; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
 ; NUMBER OF SEQUENCES: 716  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
 ; STREET: 100 ABBOTT PARK ROAD  
 ; CITY: ABBOTT PARK  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60064-3500  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/467,344A  
 ; FILING DATE: 07-Jun-1995  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/424,550  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: POREMBSKI, PRISCILLA E.  
 ; REGISTRATION NUMBER: 33,207  
 ; REFERENCE/DOCKET NUMBER: 5527.PC.01  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 708-937-6365  
 ; TELEFAX: 708-938-6235

RESULT 6  
 Query Match 44.8%; Score 30; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 4 $\text{le}+05$ ; Mismatches 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FSELW 10  
 Db 2 FSBLW 6

RESULT 6  
 US-09-035-686-6  
 Sequence 6, Application US/09035686  
 Patent No. 6153391  
 GENERAL INFORMATION:  
 APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Rohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/035,686  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/424,957  
 FILING DATE: 19-APR-1995  
 APPLICATION NUMBER: US 08/277,660  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Drager, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 US-09-035-686-6

RESULT 8  
 US-09-016-061-100  
 Sequence 100, Application US/09016061  
 Patent No. 6596850  
 GENERAL INFORMATION:  
 APPLICANT: Huse, William D.  
 TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Same and Methods of Use  
 NUMBER OF SEQUENCES: 100  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell & Flores LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/016,061  
 FILING DATE: 30-JAN-1998  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/791,391  
 FILING DATE: 30-JAN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-IX 2965  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 100:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-016-061-100

Query Match 44.8%; Score 30; DB 4; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 56; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FSELW 10  
 Db 2 FSBLW 6

Db            5 YGSFYS 10

RESULT 9  
US-08-424-957-42  
Sequence 42, Application US/08424957  
Patient No. 5770377  
GENERAL INFORMATION:  
APPLICANT: Picksey, Steven M.  
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,957  
FILING DATE: 19-APR-1995  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,660  
FILING DATE: 20-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Driger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE DOCKET NUMBER: A-61228/WHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
US-08-424-957-42

Query Match      44.8%; Score 30; DB 1; Length 11;  
Best Local Similarity      100.0%; Pred. No. 72; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db            6 FSELW 10  
              |||||  
              5 FSELW 9

RESULT 11  
US-09-595-682B-10  
Sequence 10, Application US/09595682B  
Patient No. 6800483  
GENERAL INFORMATION:  
APPLICANT: Danks, Mary K.  
APPLICANT: Potter, Philip M.  
APPLICANT: Houghton, Peter J.  
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of  
TITLE OF INVENTION: Tumor Cells  
FILE REFERENCE: SJ-0005  
CURRENT APPLICATION NUMBER: US/09/595,682B  
CURRENT FILING DATE: 2000-01-15  
PRIOR APPLICATION NUMBER: 60/075,258  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: PCT/US99/03171  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Oryctolagus cuniculus  
US-09-595-682B-10  
Query Match      43.3%; Score 29; DB 4; Length 7;  
Best Local Similarity      57.1%; Pred. No. 4.1e+05; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
Db            4 SFSELW 10  
              |||||  
              1 AFSELW 7

RESULT 10  
US-09-035-686-42  
Sequence 42, Application US/09035686  
Patient No. 6153391  
GENERAL INFORMATION:  
APPLICANT: Pickley, Steven M.  
APPLICANT: Lane, David P.  
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California

RESULT 12  
US-09-620-091-28  
; Sequence 28, Application US/09620091  
; GENERAL INFORMATION:  
; APPLICANT: CWIRLA, STEVEN E.  
; APPLICANT: DUFFIN, DAVID J.  
; APPLICANT: MERRILL, BARBARA MCEOWEN  
; APPLICANT: SHATZ, PETER JOSEPH  
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY  
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED  
; FILE REFERENCE: 0300-0014  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 491  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 10  
; TYPE: PRY  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-620-091-28

Query Match 43.3%; Score 29; DB 4; Length 10;  
Best Local Similarity 71.4%; Pred. No. 97; Mismatches 5; Conservative 1; Indels 0; Gaps 0;  
Matches 5; Conservatve 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SFPSBLW 10  
Db 3 SFVVELW 9

RESULT 13  
US-09-186-958-6  
; Sequence 6, Application US/09186958B  
; Patent No. 623860  
; GENERAL INFORMATION:  
; APPLICANT: Whelihan, E. Fayette  
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19  
; FILE REFERENCE: DYX-009.0 US sequence listing  
; CURRENT APPLICATION NUMBER: US/09186,958B  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRY  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19  
; OTHER INFORMATION: binding polypeptide  
US-09-186-958-6

Query Match 41.8%; Score 28; DB 3; Length 11;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02; Mismatches 5; Conservative 0; Indels 3; Gaps 0;  
Matches 5; Conservatve 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 FFSBLWTS 12  
Db 1 FFCALWPS 8

RESULT 14  
US-09-669-271A-5  
; Sequence 6, Application US/09669271A  
; Patent No. 6291197

Search completed: August 3, 2005, 19:04:17  
Job time : 43 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model  
Run on: August 3, 2005, 18:51:56 ; Search time 151 Seconds  
(without alignments)

30.962 Million cell updates/sec

Title: US-10-088-681-2  
Perfect score: 67  
Sequence: 1 EYGSFSEELNTS 12

Scoring table: BLOSUM62  
Gapext 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters:

243143

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : Published Applications AB,\*

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5: /cgn2\_6.ptodata/2/pubcaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_5.ptodata/2/pubcaa/PCT05\_PUBCOMB.pep:\*

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9: /cgn2\_5.ptodata/2/pubcaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6.ptodata/2/pubcaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6.ptodata/2/pubcaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_5.ptodata/2/pubcaa/US09\_NEW\_PUB.pep:\*

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18: /cgn2\_6.ptodata/2/pubcaa/US10F\_PUBCOMB.pep:\*

19: /cgn2\_6.ptodata/2/pubcaa/US11\_PUBCOMB.pep:\*

20: /cgn2\_6.ptodata/2/pubcaa/US11\_NEW\_PUB.pep:\*

21: /cgn2\_6.ptodata/2/pubcaa/US60\_NEW\_PUB.pep:\*

22: /cgn2\_6.ptodata/2/pubcaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	% Match	Length	DB ID	Description
1	34	50.7	6	16	US-10-221-042-2	Sequence 2, App
2	34	50.7	8	8	US-08-424-550B-252	Sequence 257, App
3	30	44.8	10	9	US-09-214-371-35	Sequence 35, App
4	30	44.8	10	9	US-09-214-371-36	Sequence 36, App
5	30	44.8	10	10	US-09-900-590-100	Sequence 100, App
6	30	44.8	10	14	US-10-05-231-100	Sequence 100, App
7	30	44.8	10	15	US-10-463-847-100	Sequence 100, App
8	30	44.8	10	18	US-10-927-262A-35	Sequence 35, App
9	30	44.8	10	18	US-10-927-262A-36	Sequence 36, App
10	29	43.3	7	16	US-10-271-271-10	Sequence 10, App
11	29	43.3	10	17	US-10-659-207-28	Sequence 28, App

12	28	41.8	9	9	US-09-486-734A-35	Sequence 35, App
13	28	41.8	11	9	US-09-881-276-6	Sequence 6, App
14	28	41.8	11	15	US-10-417-895A-56	Sequence 56, App
15	27	40.3	6	9	US-09-214-371-83	Sequence 83, App
16	27	40.3	6	13	US-10-155-050-1	Sequence 4, App
17	27	40.3	6	13	US-10-609-217-130	Sequence 1, App
18	27	40.3	6	15	US-10-632-389-130	Sequence 130, App
19	27	40.3	6	16	US-10-340-179-2	Sequence 130, App
20	27	40.3	6	15	US-10-651-723-130	Sequence 130, App
21	27	40.3	6	15	US-10-662-389-143	Sequence 130, App
22	27	40.3	9	9	US-09-214-371-37	Sequence 37, App
23	27	40.3	9	9	US-09-214-371-38	Sequence 38, App
24	27	40.3	9	16	US-10-645-784-130	Sequence 130, App
25	27	40.3	9	18	US-10-927-262A-83	Sequence 130, App
26	27	40.3	9	18	US-10-340-179-2	Sequence 130, App
27	27	40.3	10	17	US-10-262-334-107	Sequence 130, App
28	27	40.3	11	10	US-09-840-085-31	Sequence 130, App
29	27	40.3	12	9	US-09-214-371-17	Sequence 130, App
30	27	40.3	12	9	US-09-214-371-24	Sequence 130, App
31	27	40.3	9	18	US-10-927-262A-37	Sequence 130, App
32	27	40.3	9	18	US-10-340-179-2	Sequence 130, App
33	27	40.3	10	17	US-10-262-334-107	Sequence 130, App
34	27	40.3	11	10	US-09-840-085-31	Sequence 130, App
35	27	40.3	12	9	US-09-214-371-17	Sequence 130, App
36	27	40.3	12	9	US-09-214-371-24	Sequence 130, App
37	27	40.3	12	9	US-09-214-371-25	Sequence 130, App
38	27	40.3	12	15	US-10-609-217-132	Sequence 130, App
39	27	40.3	12	15	US-10-609-217-131	Sequence 130, App
40	27	40.3	12	15	US-10-609-217-143	Sequence 130, App
41	27	40.3	12	15	US-10-651-723-132	Sequence 130, App
42	27	40.3	12	15	US-10-652-389-131	Sequence 130, App
43	27	40.3	12	15	US-10-632-389-132	Sequence 130, App
44	27	40.3	12	15	US-10-632-389-143	Sequence 130, App
45	27	40.3	12	15	US-10-632-389-144	Sequence 130, App
46	27	40.3	12	15	US-10-651-723-131	Sequence 130, App
47	27	40.3	12	15	US-10-651-723-132	Sequence 130, App
48	27	40.3	12	15	US-10-651-723-143	Sequence 130, App
49	27	40.3	12	15	US-10-551-723-144	Sequence 130, App
50	27	40.3	12	15	US-10-551-723-144	Sequence 130, App
51	27	40.3	12	15	US-10-645-761-132	Sequence 130, App
52	27	40.3	12	15	US-10-645-761-132	Sequence 130, App
53	27	40.3	12	15	US-10-645-761-144	Sequence 130, App
54	27	40.3	12	15	US-10-666-698-131	Sequence 130, App
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60	27	40.3	12	15	US-10-653-040-143	Sequence 130, App
61	27	40.3	12	15	US-10-653-040-144	Sequence 130, App
62	27	40.3	12	15	US-10-645-784-131	Sequence 130, App
63	27	40.3	12	15	US-10-645-784-132	Sequence 130, App
64	27	40.3	12	18	US-10-645-784-143	Sequence 130, App
65	27	40.3	12	18	US-10-645-784-144	Sequence 130, App
66	27	40.3	12	18	US-10-227-262A-17	Sequence 130, App
67	27	40.3	12	18	US-10-227-262A-24	Sequence 130, App
68	27	40.3	12	18	US-10-927-262A-25	Sequence 130, App
69	26	38.8	5	9	US-09-940-605-13	Sequence 130, App
70	26	38.8	5	13	US-10-014-716-13	Sequence 130, App
71	26	38.8	5	14	US-10-259-391-13	Sequence 130, App
72	26	38.8	5	14	US-10-900-951-13	Sequence 130, App
73	26	38.8	5	14	US-10-033-195B-12	Sequence 130, App
74	26	38.8	5	17	US-10-928-299-13	Sequence 130, App
75	26	38.8	5	17	US-10-996-767-13	Sequence 130, App
76	26	38.8	7	14	US-10-321-678-12	Sequence 130, App
77	26	38.8	8	15	US-10-387-957-36	Sequence 130, App
78	26	38.8	8	15	US-10-387-957-37	Sequence 130, App
79	26	38.8	8	15	US-10-387-957-38	Sequence 130, App
80	26	38.8	8	15	US-10-387-957-39	Sequence 130, App
81	26	38.8	8	15	US-10-387-957-39	Sequence 130, App
82	26	38.8	8	15	US-10-387-957-36	Sequence 130, App
83	26	38.8	8	15	US-10-387-957-37	Sequence 130, App
84	26	38.8	8	15	US-10-387-957-38	Sequence 130, App
85	26	38.8	8	15	US-10-387-957-39	Sequence 130, App

85 26 38.8 8 16 US-10-387-955-36 Sequence 36, Appl  
 86 26 38.8 8 16 US-10-387-955-37 Sequence 37, Appl  
 87 26 38.8 8 16 US-10-387-955-38 Sequence 38, Appl  
 88 26 38.8 8 16 US-10-387-955-39 Sequence 39, Appl  
 89 26 38.8 8 16 US-10-488-219-36 Sequence 36, Appl  
 90 26 38.8 8 16 US-10-488-219-37 Sequence 37, Appl  
 91 26 38.8 8 16 US-10-488-219-38 Sequence 38, Appl  
 92 26 38.8 8 16 US-10-488-219-39 Sequence 39, Appl  
 93 26 38.8 10 10 US-09-900-590-66 Sequence 66, Appl  
 94 26 38.8 10 10 US-09-900-590-98 Sequence 98, Appl  
 95 26 38.8 10 10 US-09-750-754-74 Sequence 74, Appl  
 96 26 38.8 10 14 US-10-305-231-66 Sequence 66, Appl  
 97 26 38.8 10 14 US-10-305-231-98 Sequence 98, Appl  
 98 26 38.8 10 15 US-10-463-847-66 Sequence 66, Appl  
 99 26 38.8 10 15 US-10-463-847-98 Sequence 98, Appl  
 100 26 38.8 11 10 US-09-988-493-181 Sequence 181, App

**ALIGNMENTS**

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RESULT 1  
 US-10-221-042-2  
 ; Sequence 2, Application US/10221042  
 ; Publication No. US20040120946A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KABEKA CORPORATION  
 ; TITLE OF INVENTION: ADSORBENTS FOR DILATED CARDIOMYOPATHY  
 ; FILE REFERENCES: 12218/5  
 ; CURRENT APPLICATION NUMBER: US/10/221.042  
 ; CURRENT FILING DATE: 2002-10-09  
 ; PRIOR APPLICATION NUMBER: PCT/JP01/03026  
 ; PRIOR FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: JP 2000-106915  
 ; PRIOR FILING DATE: 2000-04-07  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: peptide  
 ; NAME/KEY: MISC\_FEATURE  
 ; OTHER INFORMATION: Peptide having a binding affinity for an antibody against M2 muscarinic receptor  
 ; OTHER INFORMATION: betat-1-adrenoceptor and/or an antibody against M2 muscarinic receptor  
 ; OTHER INFORMATION: tor  
 ; US-10-221-042-2

Query Match 50.7%; Score 34; DB 16; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Other 0;

Oy 1 EYGSFF 6  
 Db 1 EYGSFF 6

RESULT 2  
 US-08-424-550B-252  
 ; Sequence 252, Application US/08424550B  
 ; Publication No. US2002011947A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JOHN N. SIMONS  
 ; APPLICANT: TAMI J. PILOT-MATIAS  
 ; APPLICANT: GEORGE J. DAWSON  
 ; APPLICANT: GEORGE G. SCHLAUDER  
 ; APPLICANT: SURESH M. DESAI  
 ; APPLICANT: THOMAS P. LEARY  
 ; APPLICANT: ANTHONY SCOTT MURSHOFF  
 ; APPLICANT: JAMES C. ERKER  
 ; APPLICANT: SHERI L. BUIJK

Query Match 50.7%; Score 34; DB 8; Length 8;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+06; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Other 0;

Oy 6 FSLBLWTS 12  
 Db 1 FSLBLWTS 7

RESULT 3  
 US-09-214-371-35  
 ; Sequence 35, Application US/09214371B  
 ; Patent No. US2001018851A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lane, David  
 ; APPLICANT: Bottger, Volker  
 ; APPLICANT: Bottger, Angelica  
 ; APPLICANT: Pickaley, Stephen  
 ; APPLICANT: Chene, Patrick  
 ; APPLICANT: Hochkeppel, Heinz-Kurt  
 ; APPLICANT: Garcia-Echeverria, Carlos  
 ; APPLICANT: Furet, Pascal  
 ; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2  
 ; FILE REFERENCE: 4-2093/A/PCT  
 ; CURRENT APPLICATION NUMBER: US/09/214.371B  
 ; CURRENT FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
 ; PRIOR FILING DATE: 1997-07-04  
 ; NUMBER OF SEQ ID NOS: 83  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 35  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:peptide  
 ; NAME/KEY: VARIANT  
 ; LOCATION: (1)

OTHER INFORMATION: X = Acc-Cys (Acrd)

NAME/KEY: VARIANT

LOCATION: (10)

OTHER INFORMATION: X = Pro-NH2

US-09-214-371-35

Query Match ; OTHER INFORMATION: Best Local Similarity 62.5%; Pred. No. 2.8e+02; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GSFFSELW 10  
Db 2 GPFPSDLW 9

RESULT 4 US-09-214-371-36

; Sequence 36, Application US/09214371B

; Patent No. US201001008511A1

; GENERAL INFORMATION:

; APPLICANT: Lan, David

; APPLICANT: Bottger, Volker

; APPLICANT: Bottger, Angelica

; APPLICANT: Picklesy, Stephen

; APPLICANT: Chene, Patrick

; APPLICANT: Hochkeppel, Hein-Kurt

; APPLICANT: Garcia-Echeverria, Carlos

; APPLICANT: Forst, Pascal

; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2.

; CURRENT FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: PCT/EP97/03549

; PRIOR FILING DATE: 1997-07-04

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 36

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:peptide

; NAME/KEY: VARIANT

; LOCATION: (1)

; OTHER INFORMATION: X = AC-Cys

; NAME/KEY: VARIANT

; LOCATION: (10)

; OTHER INFORMATION: X = Pro-NH2

; US-09-214-371-36

Query Match ; OTHER INFORMATION: Best Local Similarity 44.8%; Score 30; DB 9; Length 10; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GSFFSELW 10  
Db 2 GPFPSDLW 9

RESULT 5 US-09-900-590-100

; Sequence 100, Application US/09900590

; Publication No. US200302800941

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic Acid Encoding Same and Methods of Use

; FILE REFERENCE: P-IX 336

; CURRENT APPLICATION NUMBER: US/10/305,231

; CURRENT FILING DATE: 2002-11-25

; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/09/339,922

; PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-24

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 100

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Mutated CDR

; OTHER INFORMATION: Complementarity determining region (CDR)

; US-10-305-231-100

Query Match ; OTHER INFORMATION: Best Local Similarity 44.8%; Score 30; DB 14; Length 10; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGSFSPS 7  
Db 5 YGSFV 10



RESULT 10  
 US-10-58-271-10  
 ; Sequence 10, Application US/10858271  
 ; Publication No. US20040259829A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Danko, Mary K.  
 ; APPLICANT: Porter, Philip M.  
 ; APPLICANT: Houghton, Peter J.  
 ; TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of  
 ; FILE REFERENCE: SJ-0005  
 ; CURRENT APPLICATION NUMBER: US/10/858,271  
 ; CURRENT FILING DATE: 2004-06-01  
 ; PRIOR APPLICATION NUMBER: US/09/595,682  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: 60/075,258  
 ; PRIOR FILING DATE: 1998-02-19  
 ; PRIOR APPLICATION NUMBER: PCT/US99/03171  
 ; PRIOR FILING DATE: 1999-02-12  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Oryctolagus cuniculus  
 ; US-10-58-271-10

Query Match 43.3%; Score 29; DB 16; Length 7;  
 Best Local Similarity 57.1%; Pred. No. 1.6e+06;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 SPFSELW 10  
 Db 1 AFNTELW 7

RESULT 11  
 US-10-59-207-28  
 ; Sequence 28, Application US/10659207  
 ; Publication No. US20050037959A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CWRILA, STEVEN E.  
 ; APPLICANT: BALU, PALANI  
 ; APPLICANT: DUFFIN, DAVID J.  
 ; APPLICANT: PIPPLANI, SUNIL  
 ; APPLICANT: MERRILL, BARBARA MCEOWEN  
 ; APPLICANT: SCHARTZ, PETER JOSEPH  
 ; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY  
 ; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED  
 ; TITLE OF INVENTION: USES  
 ; FILE REFERENCE: 0300-0014  
 ; CURRENT APPLICATION NUMBER: US/10/659,207  
 ; CURRENT FILING DATE: 2003-09-09  
 ; PRIOR APPLICATION NUMBER: US/09/620,091  
 ; PRIOR FILING DATE: 2000-07-20  
 ; NUMBER OF SEQ ID NOS: 491  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 28  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; US-10-659-207-28

Query Match 43.3%; Score 29; DB 17; Length 10;  
 Best Local Similarity 71.4%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 12  
 US-09-486-734A-35  
 ; Sequence 35, Application US/09486734A  
 ; Patent No. US2002016732A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chopin, Marie-Christine  
 ; APPLICANT: Cler, Florence  
 ; APPLICANT: Erlih, S. Dusko  
 ; APPLICANT: Gautier, Michel  
 ; APPLICANT: Schouler, Catherine  
 ; APPLICANT: Institut National de la Recherche Agronomique  
 ; TITLE OF INVENTION: Resistance Mechanisms to IC Type R/M  
 ; TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria  
 ; FILE REFERENCE: 33339/196048  
 ; CURRENT APPLICATION NUMBER: US/09/486,734A  
 ; CURRENT FILING DATE: 2000-05-03  
 ; PRIOR APPLICATION NUMBER: PCT/FR98/01873  
 ; PRIOR FILING DATE: 1998-09-01  
 ; PRIOR APPLICATION NUMBER: FR 97/10885  
 ; PRIOR FILING DATE: 1997-09-02  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: FastaSeq for Windows Version 4.0  
 ; SEQ ID NO 35  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Hsds subunit  
 ; US-09-486-734A-35

QY 3 GSFFSELJ 9  
 Db 2 GSFFKQL 8

RESULT 13  
 US-09-881-276-5  
 ; Sequence 6, Application US/09881276  
 ; Patent No. US20020031761A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Whelihan, E. Fayelle  
 ; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19  
 ; FILE REFERENCE: DIX-009.0 US-2  
 ; CURRENT APPLICATION NUMBER: US/09/881,276  
 ; CURRENT FILING DATE: 2001-06-14  
 ; PRIOR APPLICATION NUMBER: 09/669,271  
 ; PRIOR FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: 09/186,958  
 ; PRIOR FILING DATE: 1998-11-05  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: Microsoft Word 97  
 ; SEQ ID NO 6  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypept  
 ; US-09-881-276-6

Query Match 41.8%; Score 28; DB 9; Length 11;  
 Best Local Similarity 62.5%; Pred. No. 6.7e+02;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      5 FFSEBLWTS 12
      ||||| |
      1 FPCALWPS 8
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QY      6 FSEBLW 10
      ||:|| |
      2 FSDLW 6
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RESULT 14  
US-10-417-895A-56

; Sequence 56, Application US/10417895A

; Publication No. US20040033569A1

; GENERAL INFORMATION:

; APPLICANT: Crea, Roberto

; APPLICANT: Cappuccilli, Guido

; TIME OF INVENTION: "DOPING IN WALK-THROUGH MUTAGENESIS

; FILE REFERENCE: 1551\_2002-001

; CURRENT APPLICATION NUMBER: US/10417,895A

; CURRENT FILING DATE: 2003-04-16

; PRIOR APPLICATION NUMBER: 60/373,886

; PRIOR FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 56

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: variant peptide for third complementarity

; OTHER INFORMATION: determining region of Fv region of an

; OTHER INFORMATION: immunoglobulin

US-10-417-895A-56

; Query Match

; Best Local Similarity 41.8%; Score 28; DB 15; Length 11;

; Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 SFSEBLWTS 12
 ||:|| |:|
 1 SYSSSSWSS 9

RESULT 15  
US-09-214-371-83

; Sequence 83, Application US/09214371B

; Patent No. US2001018511A1

; GENERAL INFORMATION:

; APPLICANT: Lane, David

; APPLICANT: Bottger, Volker

; APPLICANT: Bottger, Angelica

; APPLICANT: Picklesley, Stephen

; APPLICANT: Chene, Patrick

; APPLICANT: Hochkeppel, Heinz-Kurt

; APPLICANT: Garcia-Echeverria, Carlos

; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2

; FILE REFERENCE: 4-20937/A/PCT

; CURRENT APPLICATION NUMBER: US/09/214,371B

; CURRENT FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: PCT/EP97/03549

; PRIOR FILING DATE: 1997-07-04

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 83

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: Description of Artificial Sequence:peptide, amin

; OTHER INFORMATION: Description of Artificial Sequence:peptide, amin

US-09-214-371-83

Search completed: August 3, 2005, 19:03:29  
Job time : 152 SECs

Query Match 40.3%; Score 27; DB 9; Length 6;  
Best Local Similarity 80.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;